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# LAMMPS Documentation

(17 July 2006 version of LAMMPS)

LAMMPS stands for Large-scale Atomic/Molecular Massively Parallel Simulator.

LAMMPS is a classical molecular dynamics simulation code designed to run efficiently on parallel computers. It was developed at Sandia National Laboratories, a US Department of Energy facility, with funding from the DOE. It is an open-source code, distributed freely under the terms of the GNU Public License (GPL).

The primary author of the code is [Steve Plimpton](mailto:sjplimp@sandia.gov), who can be contacted at [sjplimp@sandia.gov](mailto:sjplimp@sandia.gov). The [LAMMPS WWW Site](http://www.cs.sandia.gov/~sjplimp/lammps.html) at [www.cs.sandia.gov/~sjplimp/lammps.html](http://www.cs.sandia.gov/~sjplimp/lammps.html) has more information about the code and its uses.

---

The LAMMPS documentation is organized into the following sections. If you find errors or omissions in this manual or have suggestions for useful information to add, please send us an [email](#) so we can improve the LAMMPS documentation.

[PDF file](#) of the entire manual, generated by [htmldoc](#)

1. [Introduction](#)
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## 1. Introduction

These sections provide an overview of what LAMMPS can and can't do, describe what it means for LAMMPS to be an open-source code, and acknowledge the funding and people who have contributed to LAMMPS over the years.

- 1.1 [What is LAMMPS](#)
  - 1.2 [LAMMPS features](#)
  - 1.3 [LAMMPS non-features](#)
  - 1.4 [Open source distribution](#)
  - 1.5 [Acknowledgments and citations](#)
- 

### 1.1 What is LAMMPS

LAMMPS is a classical molecular dynamics code that models an ensemble of particles in a liquid, solid, or gaseous state. It can model atomic, polymeric, biological, metallic, or granular systems using a variety of force fields and boundary conditions.

For examples of LAMMPS simulations, see the Publications page of the [LAMMPS WWW Site](#).

LAMMPS runs efficiently on single-processor desktop or laptop machines, but is designed for parallel computers. It will run on any parallel machine that compiles C++ and supports the [MPI](#) message-passing library. This includes distributed- or shared-memory parallel machines and Beowulf-style clusters.

LAMMPS can model systems with only a few particles up to millions or billions. See [this section](#) for information on LAMMPS performance and scalability, or the Benchmarks section of the [LAMMPS WWW Site](#).

LAMMPS is a freely-available open-source code, distributed under the terms of the [GNU Public License](#), which means you can use or modify the code however you wish. See [this section](#) for a brief discussion of the open-source philosophy.

LAMMPS is designed to be easy to modify or extend with new capabilities, such as new force fields, atom types, boundary conditions, or diagnostics. See [this section](#) for more details.

The current version of LAMMPS is written in C++. Earlier versions were written in F77 and F90. See [this section](#) for more information on different versions. All versions can be downloaded from the [LAMMPS WWW Site](#).

LAMMPS was originally developed under a US Department of Energy CRADA (Cooperative Research and Development Agreement) between two DOE labs and 3 companies. It is distributed by [Sandia National Labs](#). See [this section](#) for more information on LAMMPS funding and individuals who have contributed to LAMMPS.

In the most general sense, LAMMPS integrates Newton's equations of motion for collections of atoms, molecules, or macroscopic particles that interact via short- or long-range forces with a variety of initial and/or boundary conditions. For computational efficiency LAMMPS uses neighbor lists to keep track of nearby particles. The lists are optimized for systems with particles that are repulsive at short distances, so that the local density of particles never becomes too large. On parallel machines, LAMMPS uses spatial-decomposition techniques to partition the simulation domain into small 3d sub-domains, one of which is assigned to each processor. Processors communicate and store "ghost" atom information for atoms that border their sub-domain. LAMMPS is most efficient (in a parallel sense) for systems whose particles fill a 3d rectangular box with roughly uniform density. Papers with technical details of the algorithms used in LAMMPS are listed in [this section](#).

---

## 1.2 LAMMPS features

This section highlights LAMMPS features, with pointers to specific commands which give more details. If LAMMPS doesn't have your favorite interatomic potential, boundary condition, or atom type, see [this section](#), which describes how you can add it to LAMMPS.

### Kinds of systems LAMMPS can simulate:

([atom style](#) command)

- atomic (e.g. box of Lennard-Jonesium)
- bead-spring polymers
- united-atom polymers or organic molecules
- all-atom polymers, organic molecules, proteins, DNA
- metals
- granular materials
- hybrid systems

### Force fields:

([pair style](#), [bond style](#), [angle style](#), [dihedral style](#), [improper style](#), [kspace style](#) commands)

- pairwise potentials: Lennard-Jones, Coulombic, Buckingham, Morse, Yukawa, embedded atom method (EAM, Finnis/Sinclair), frictional granular,
- Debye, soft, DPD, class 2 (COMPASS), tabulated, hybrid
- bond potentials: harmonic, FENE, Morse, nonlinear, class 2, quartic (breakable), hybrid
- angle potentials: harmonic, CHARMM, cosine, cosine/squared, class 2 (COMPASS), hybrid
- dihedral potentials: harmonic, CHARMM, multi-harmonic, helix, class 2 (COMPASS), OPLS, hybrid
- improper potentials: harmonic, cvff, class 2 (COMPASS), hybrid

- polymer potentials: all-atom, united-atom, bead-spring, breakable
- water potentials: TIP3P, TIP4P, SPC
- long-range Coulombics: Ewald, PPPM (similar to particle-mesh Ewald)
- CHARMM, AMBER, OPLS force-field compatibility

### Creation of atoms:

(read\_data, lattice, create\_atoms, delete\_atoms, displace\_atoms commands)

- read in atom coords from files
- create atoms on one or more lattices (e.g. grain boundaries)
- delete geometric or logical groups of atoms (e.g. voids)
- displace atoms

### Ensembles, constraints, and boundary conditions:

(fix command)

- constant NVE, NVT, NPT, NPH integrators
- thermostatting options for groups and geometric regions of atoms
- pressure control via Nose/Hoover barostatting in 1 to 3 dimensions
- volume rescaling
- altered motion via velocity and force constraints
- harmonic (umbrella) constraint forces
- dragging of atoms to new positions
- independent or coupled rigid body integration
- SHAKE bond and angle constraints
- wall constraints of various kinds
- targeted molecular dynamics (TMD) constraints
- gravity

### Integrators:

(run, run\_style, temper commands)

- velocity-Verlet integrator
- Brownian dynamics
- energy minimization via conjugate gradient relaxation
- rRESPA hierarchical timestepping
- parallel tempering (replica exchange)
- multiple independent simulations simultaneously

### Output:

(dump, restart commands)

- binary restart files
- text dump files of atom coords, velocities, other per-atom attributes
- atom snapshots in native, XYZ, XTC, DCD formats
- per-atom energy, stress, centro-symmetry parameter

## Pre- and post-processing:

Our group has also written and released a separate toolkit called [Pizza.py](#) which provides tools for doing setup, analysis, plotting, and visualization for LAMMPS simulations. Pizza.py is written in [Python](#) and is available for download from [the Pizza.py WWW site](#).

---

### 1.3 LAMMPS non-features

LAMMPS is designed to efficiently compute Newton's equations of motion for a system of interacting particles. Many of the tools needed to pre- and post-process the data for such simulations are not included in the LAMMPS kernel for several reasons:

- the desire to keep LAMMPS simple
- they are not parallel operations
- other codes already do them
- limited development resources

Specifically, LAMMPS itself does not:

- run thru a GUI
- build molecular systems
- assign force-field coefficients automatically
- perform sophisticated analyses of your MD simulation
- visualize your MD simulation
- plot your output data

A few tools for pre- and post-processing tasks are provided as part of the LAMMPS package; they are described in [this section](#). However, many people use other codes or write their own tools for these tasks.

As noted above, our group has also written and released a separate toolkit called [Pizza.py](#) which addresses some of the listed bullets. It provides tools for doing setup, analysis, plotting, and visualization for LAMMPS simulations. Pizza.py is written in [Python](#) and is available for download from [the Pizza.py WWW site](#).

LAMMPS requires as input a list of initial atom coordinates and types, molecular topology information, and force-field coefficients assigned to all atoms and bonds. LAMMPS will not build molecular systems and assign force-field parameters for you.

For atomic systems LAMMPS provides a [create atoms](#) command which places atoms on solid-state lattices (fcc, bcc, etc). Assigning small numbers of force field coefficients can be done via the [pair coeff](#), [bond coeff](#), [angle coeff](#), etc commands. For molecular systems or more complicated simulation geometries, users typically use another code as a builder and convert its output to LAMMPS input format, or write their own code to generate atom coordinate and molecular topology for LAMMPS to read in.

For complicated molecular systems (e.g. a protein), a multitude of topology information and hundreds of force-field coefficients must typically be specified. We suggest you use a program like [CHARMM](#) or [AMBER](#) or other molecular builders to setup such problems and dump its information to a file. You can then reformat the file as LAMMPS input. Some of the tools in [this section](#) can assist in this process.

Similarly, LAMMPS creates output files in a simple format. Most users post-process these files with their own analysis tools or re-format them for input into other programs, including visualization packages. If you



are convinced you need to compute something on-the-fly as LAMMPS runs, see [this section](#) for a discussion of how you can use the [dump](#) and [fix](#) commands to print out data of your choosing. Keep in mind that complicated computations can slow down the molecular dynamics timestepping, particularly if the computations are not parallel, so it is often better to leave such analysis to post-processing codes.

A very simple (yet fast) visualizer is provided with the LAMMPS package – see the [xmovie](#) tool in [this section](#). It creates xyz projection views of atomic coordinates and animates them. We find it very useful for debugging purposes. For high-quality visualization we recommend the following packages:

- [Raster3d](#)
- [RasMol](#)
- [VMD](#)
- [AtomEye](#)

Other features that LAMMPS does not yet (and may never) support are discussed in [this section](#).

Finally, these are freely-available molecular dynamics codes, most of them parallel, which may be well-suited to the problems you want to model. They can also be used in conjunction with LAMMPS to perform complementary modeling tasks.

- [CHARMM](#)
- [AMBER](#)
- [NAMD](#)
- [NWCHEM](#)
- [DL\\_POLY](#)
- [Tinker](#)

CHARMM, AMBER, NAMD, NWCHEM, and Tinker are designed primarily for modeling biological molecules. CHARMM and AMBER use atom-decomposition (replicated-data) strategies for parallelism; NAMD and NWCHEM use spatial-decomposition approaches, similar to LAMMPS. Tinker is a serial code. DL\_POLY includes potentials for a variety of biological and non-biological materials; both a replicated-data and spatial-decomposition version exist.

---

## 1.4 Open source distribution

LAMMPS comes with no warranty of any kind. As each source file states in its header, it is a copyrighted code that is distributed free-of-charge, under the terms of the [GNU Public License](#) (GPL). This is often referred to as open-source distribution – see [www.gnu.org](http://www.gnu.org) or [www.opensource.org](http://www.opensource.org) for more details. The legal text of the GPL is in the LICENSE file that is included in the LAMMPS distribution.

Here is a summary of what the GPL means for LAMMPS users:

- (1) Anyone is free to use, modify, or extend LAMMPS in any way they choose, including for commercial purposes.
- (2) If you distribute a modified version of LAMMPS, it must remain open-source, meaning you distribute it under the terms of the GPL. You should clearly annotate such a code as a derivative version of LAMMPS.
- (3) If you release any code that includes LAMMPS source code, then it must also be open-sourced, meaning you distribute it under the terms of the GPL.

(4) If you give LAMMPS files to someone else, the GPL LICENSE file and source file headers (including the copyright and GPL notices) should remain part of the code.

In the spirit of an open-source code, these are various ways you can contribute to making LAMMPS better. You can send email on any of these items.

- Point prospective users to the LAMMPS WWW Site. Mention it in talks or link to it from your WWW site.
- If you find an error or omission in this manual or on the LAMMPS WWW Site, or have a suggestion for something to clarify or include, send an email.
- If you find a bug, this section describes how to report it.
- If you publish a paper using LAMMPS results, send the citation (and any cool pictures or movies if you like) to add to the Publications, Pictures, and Movies pages of the LAMMPS WWW Site, with links and attributions back to you.
- Create a new Makefile.machine that can be added to the src/MAKE directory.
- The tools sub-directory of the LAMMPS distribution has various stand-alone codes for pre- and post-processing of LAMMPS data. More details are given in this section. If you write a new tool that users will find useful, it can be added to the LAMMPS distribution.
- LAMMPS is designed to be easy to extend with new code for features like potentials, boundary conditions, diagnostic computations, etc. This section gives details. If you add a feature of general interest, it can be added to the LAMMPS distribution.
- The Benchmark page of the LAMMPS WWW Site lists LAMMPS performance on various platforms. The files needed to run the benchmarks are part of the LAMMPS distribution. If your machine is sufficiently different from those listed, your timing data can be added to the page.
- You can send feedback for the User Comments page of the LAMMPS WWW Site. It might be added to the page. No promises.
- Cash. Small denominations, unmarked bills preferred. Paper sack OK. Leave on desk. VISA also accepted. Chocolate chip cookies encouraged.

---

## 1.5 Acknowledgments and citations

LAMMPS development has been funded by the US Department of Energy (DOE), through its CRADA, LDRD, ASCI, and Genomes-to-Life programs and its OASCR and OBER offices.

Specifically, work on the latest version was funded in part by the US Department of Energy's Genomics:GTL program (www.doegenomestolife.org) under the project, "Carbon Sequestration in Synechococcus Sp.: From Molecular Machines to Hierarchical Modeling".

The following papers describe the parallel algorithms used in LAMMPS.

S. J. Plimpton, **Fast Parallel Algorithms for Short-Range Molecular Dynamics**, J Comp Phys, 117, 1–19 (1995).

S. J. Plimpton, R. Pollock, M. Stevens, **Particle-Mesh Ewald and rRESPA for Parallel Molecular Dynamics Simulations**, in Proc of the Eighth SIAM Conference on Parallel Processing for Scientific Computing, Minneapolis, MN (March 1997).

If you use LAMMPS results in your published work, please cite the J Comp Phys reference and include a pointer to the LAMMPS WWW Site (www.cs.sandia.gov/~sjplimp/lammps.html). A paper describing the latest version of LAMMPS is in the works; when it appears in print, you can check the LAMMPS WWW Site for a more current citation.

If you send me information about your publication, I'll be pleased to add it to the Publications page of the [LAMMPS WWW Site](#). Ditto for a picture or movie for the Pictures or Movies pages.

The primary author of LAMMPS is [Steve Plimpton](#) at Sandia National Labs. Others have made significant contributions to the code:

|  |   |
|--|---|
| Ewald and PPPM solvers                 | Roy Pollock (LLNL)  |
| rRESPA                                 | Mark Stevens & Paul Crozier (Sandia)                                  |
| NVT/NPT integrators                    | Mark Stevens (Sandia)   |
| class 2 force fields                   | Eric Simon (Cray)   |
| HTFN energy minimizer                  | Todd Plantenga (Sandia)   |
| msi2lmp tool                           | Steve Lustig (Dupont), Mike Peachey & John Carpenter (Cray)           |
| CHARMM force fields                    | Paul Crozier (Sandia)   |
| 2d Ewald/PPPM                          | Paul Crozier (Sandia)   |
| granular force fields and BC           | Leo Silbert & Gary Grest (Sandia)                                     |
| multi-harmonic dihedral potential      | Mathias Putz (Sandia)   |
| EAM potentials                         | Stephen Foiles (Sandia)   |
| parallel tempering                     | Mark Sears (Sandia)   |
| lmp2cfg and lmp2traj tools             | Ara Kooser, Jeff Greathouse, Andrey Kalinichev (Sandia)               |
| FFT support for SGI SCLS (Altix)       | Jim Shepherd (Ga Tech)  |
| targeted molecular dynamics (TMD)      | Paul Crozier (Sandia), Christian Burisch (Bochum University, Germany) |
| force tables for long-range Coulombics | Paul Crozier (Sandia)   |
|  |   |

|  |  |
|--|--|
| radial distribution functions                  | Paul Crozier & Jeff Greathouse (Sandia)                            |
| Morse bond potential                           | Jeff Greathouse (Sandia)   |
| CHARMM LAMMPS tool                             | Pieter in't Veld and Paul Crozier (Sandia)                         |
| AMBER LAMMPS tool                              | Keir Novik (Univ College London) and Vikas Varshney (U Akron)      |
| electric field fix                             | Christina Payne (Vanderbilt U)                                     |
| cylindrical indenter fix                       | Ravi Agrawal (Northwestern U)                                      |
| compressed dump files                          | Erik Luijten (U Illinois)  |
| thermodynamics enhanced by fix quantities      | Aidan Thompson (Sandia)  |
| uniaxial strain fix                            | Carsten Svaneborg (Max Planck Institute)                           |
| TIP4P potential (4-site water)                 | Ahmed Ismail and Amalie Frischknecht (Sandia)                      |
| dissipative particle dynamics (DPD) potentials | Kurt Smith (U Pitt) and Frank van Swol (Sandia)                    |
| Finnis/Sinclair EAM                            | Tim Lau (MIT)  |
| helix dihedral potential                       | Naveen Michaud-Agrawal (Johns Hopkins U) and Mark Stevens (Sandia) |
| cosine/squared angle potential                 | Naveen Michaud-Agrawal (Johns Hopkins U)                           |
| EAM CoAl and AlCu potentials                   | Kwang-Reoul Lee (KIST, Korea)                                      |
| self spring fix                                | Naveen Michaud-Agrawal (Johns Hopkins U)                           |

|   |  |
|---|--|
| radius-of-gyration<br>spring fix          | Naveen<br>Michaud-Agrawal<br>(Johns Hopkins U)<br>and Paul Crozier<br>(Sandia)   |
| lj/smooth pair<br>potential               | Craig Maloney<br>(UCSB)  |
| grain boundary<br>orientation fix         | Koenraad Janssens<br>and David Olmsted<br>(SNL)  |
| DCD and XTC<br>dump styles                | Naveen<br>Michaud-Agrawal<br>(Johns Hopkins U)   |
| breakable bond<br>quartic potential       | Chris Lorenz and<br>Mark Stevens<br>(SNL)  |
| faster pair hybrid<br>potential           | James Fischer<br>(High Performance<br>Technologies, Inc),<br>Vincent Natoli and<br>David Richie<br>(Stone Ridge<br>Technology) |
| POEMS coupled<br>rigid body<br>integrator | Rudranarayan<br>Mukherjee (RPI)  |

Other CRADA partners involved in the design and testing of LAMMPS were

- John Carpenter (Mayo Clinic, formerly at Cray Research)
- Terry Stouch (Lexicon Pharmaceuticals, formerly at Bristol Myers Squibb)
- Steve Lustig (Dupont)
- Jim Belak (LLNL)

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## 2. Getting Started

This section describes how to unpack, make, and run LAMMPS, for both new and experienced users.

[2.1 What's in the LAMMPS distribution](#)

[2.2 Making LAMMPS](#)

[2.3 Running LAMMPS](#)

[2.4 Command-line options](#)

[2.5 Screen output](#)

[2.6 Tips for users of previous versions](#)

## 2.1 What's in the LAMMPS distribution

When you download LAMMPS you will need to unzip and untar the downloaded file with the following commands, after placing the file in an appropriate directory.

```
gunzip lammeps*.tar.gz
tar xvf lammeps*.tar
```

This will create a LAMMPS directory containing two files and several sub-directories:

|            |  |
|------------|--|
| README     | text file  |
| LICENSE    | the GNU<br>General Public<br>License (GPL)       |
| bench      | benchmark<br>problems                            |
| doc        | documentation                                    |
| examples   | simple test<br>problems                          |
| potentials | embedded atom<br>method (EAM)<br>potential files |
| src        | source files                                     |
| tools      | pre- and<br>post-processing<br>tools             |

---

## 2.2 Making LAMMPS

### *Read this first:*

Building LAMMPS can be non-trivial. You will likely need to edit a makefile, there are compiler options, additional libraries can be used (MPI, FFT), etc. Please read this section carefully. If you are not comfortable with makefiles, or building codes on a Unix platform, or running an MPI job on your machine, please find a local expert to help you. Many of the emails I get about build and run problems are not really about LAMMPS – they are peculiar to the user's system, compilers, libraries, etc. Such questions are better answered by a local expert.

If you have a build problem that you are convinced is a LAMMPS issue (e.g. the compiler complains about a line of LAMMPS source code), then please send an [email](#). Note that doesn't include linking problems – that's a question for a local expert!

Also, if you succeed in building LAMMPS on a new kind of machine (which there isn't a similar Makefile for in the distribution), send it to [sjplimp@sandia.gov](mailto:sjplimp@sandia.gov) and we'll include it in future LAMMPS releases.

### *Building a LAMMPS executable:*

The src directory contains the C++ source and header files for LAMMPS. It also contains a top-level Makefile and a MAKE directory with low-level Makefile.\* files for several machines. From within the src

directory, type "make" or "gmake". You should see a list of available choices. If one of those is the machine and options you want, you can type a command like:

```
make linux
gmake mac
```

If you get no errors and an executable like `lmp_linux` or `lmp_mac` is produced, you're done; it's your lucky day. The remainder of this section addressed the following topics: errors that occur when making LAMMPS, editing a new low-level `Makefile.foo`, how to make LAMMPS with and without packages, and additional build tips.

### ***Errors that occur when making LAMMPS:***

(1) If the make command breaks immediately with errors that indicate it can't find files with a "\*" in their names, this can be because your machine's make doesn't support wildcard expansion in a makefile. Try `gmake` instead of `make`. If that doesn't work, try using a `-f` switch with your make command to use `Makefile.list` which explicitly lists all the needed files, e.g.

```
make makelist
make -f Makefile.list linux
gmake -f Makefile.list mac
```

The first "make" command will create a current `Makefile.list` with all the file names in your `src` dir. The 2nd "make" command (`make` or `gmake`) will use it to build LAMMPS.

(2) Other errors typically occur because the low-level `Makefile` isn't setup correctly for your machine. If your platform is named "foo", you need to create a `Makefile.foo` in the `MAKE` directory. Use whatever existing file is closest to your platform as a starting point. See the next section for more instructions.

### ***Editing a new low-level Makefile.foo:***

These are the issues you need to address when editing a low-level `Makefile` for your machine. With a couple exceptions, the only portion of the file you should need to edit is the "System-specific Settings" section.

(1) Change the first line of `Makefile.foo` to include the word "foo" and whatever other options you set. This is the line you will see if you just type "make".

(2) Set the paths and flags for your C++ compiler, including optimization flags. You can use `g++`, the open-source GNU compiler, which is available on all Unix systems. Vendor compilers often produce faster code. On boxes with Intel CPUs, I use the free Intel `icc` compiler, which you can download from [Intel's compiler site](#).

(3) If you want LAMMPS to run in parallel, you must have an MPI library installed on your platform. `Makefile.foo` needs to specify where the `mpi.h` file (`-I` switch) and the `libmpi.a` library (`-L` switch) is found. On my Linux box, I use Argonne's MPICH 1.2 which can be downloaded from the [Argonne MPI site](#). LAM MPI should also work. If you are running on a big parallel platform, your system people or the vendor should have already installed a version of MPI, which will be faster than MPICH or LAM, so find out how to link against it. If you use MPICH or LAM, you will have to configure and build it for your platform. The MPI configure script should have compiler options to enable you to use the same compiler you are using for the LAMMPS build, which can avoid problems that may arise when linking LAMMPS to the MPI library.

(4) If you just want LAMMPS to run on a single processor, you can use the STUBS library in place of MPI, since you don't need an MPI library installed on your system. See the Makefile.serial file for how to specify the `-I` and `-L` switches. You will also need to build the STUBS library for your platform before making LAMMPS itself. From the STUBS dir, type "make" and it will hopefully create a libmpi.a suitable for linking to LAMMPS. If the build fails, you will need to edit the STUBS/Makefile for your platform.

The file STUBS/mpi.cpp has a CPU timer function `MPI_Wtime()` that calls `gettimeofday()`. If your system doesn't support `gettimeofday()`, you'll need to insert code to call another timer. Note that the ANSI-standard function `clock()` rolls over after an hour or so, and is therefore insufficient for timing long LAMMPS runs.

(5) If you want to use the particle-particle particle-mesh (PPPM) option in LAMMPS for long-range Coulombics, you must have a 1d FFT library installed on your platform. This is specified by a switch of the form `-DFFT_XXX` where `XXX` = INTEL, DEC, SGI, SCSL, or FFTW. All but the last one are native vendor-provided libraries. FFTW is a fast, portable library that should work on any platform. You can download it from [www.fftw.org](http://www.fftw.org). Use version 2.1.X, not the newer 3.0.X. Building FFTW for my box was as simple as `./configure; make`. Whichever FFT library you have on your platform, you'll need to set the appropriate `-I` and `-L` switches in Makefile.foo.

If you examine `fft3d.c` and `fft3d.h` you'll see it's possible to add other vendor FFT libraries via `#ifdef` statements in the appropriate places. If you successfully add a new FFT option, like `-DFFT_IBM`, please send me an email; I'd like to add it to LAMMPS.

(6) If you don't plan to use PPPM, you don't need an FFT library. Use a `-DFFT_NONE` switch in the `CCFLAGS` setting of Makefile.foo, or exclude the KSPACE package (see below).

(7) There are a few other `-D` compiler switches you can set as part of `CCFLAGS`. The `read_data` and `dump` commands will read/write gzipped files if you compile with `-DGZIP`. It requires that your Unix support the "popen" command. Using one of the `-DPACK_ARRAY`, `-DPACK_POINTER`, and `-DPACK_MEMCPY` options can make for faster parallel FFTs (in the PPPM solver) on some platforms. The `-DPACK_ARRAY` setting is the default.

(8) The `DEPFLAGS` setting is how the C++ compiler creates a dependency file for each source file. This speeds re-compilation when source (\*.cpp) or header (\*.h) files are edited. Some compilers do not support dependency file creation, or may use a different switch than `-D`. GNU g++ works with `-D`. If your compiler can't create dependency files (a long list of errors involving \*.d files), then you'll need to create a Makefile.foo patterned after Makefile.tflow, which uses different rules that do not involve dependency files.

That's it. Once you have a correct Makefile.foo and you have pre-built the MPI and FFT libraries it will use, all you need to do from the src directory is type one of these 2 commands:

```
make foo
gmake foo
```

You should get the executable `lmp_foo` when the build is complete.

### ***How to make LAMMPS with and without packages:***

The source code for LAMMPS is structured as a large set of core files that are always used plus additional packages, which are groups of files that enable a specific set of features. For example, force fields for molecular systems or granular systems are in packages. You can see the list of packages by typing "make package". The current list of packages is as follows:



|          |   |
|----------|---|
| class2   | class 2 force fields                                      |
| dpd      | dissipative particle dynamics (DPD) force field           |
| granular | force fields and boundary conditions for granular systems |
| kspace   | long-range Ewald and particle-mesh (PPPM) solvers         |
| molecule | force fields for molecular systems                        |
| poems    | coupled rigid body motion                                 |
| xtc      | dump atom snapshots in XTC format                         |

Any or all of these packages can be included or excluded when LAMMPS is built. The default is to include only the kspace and molecule packages. You may wish to exclude certain packages if you will never run certain kinds of simulations. This will produce a smaller executable which in some cases will also run a bit faster.

Packages are included or excluded by typing "make yes-name" or "make no-name", where "name" is the name of the package. You can also type "make yes-all" or "make no-all" to include/exclude all optional packages. These commands work by simply moving files back and forth between the main src directory and sub-directories with the package name, so that the files are not seen when LAMMPS is built. After you have included or excluded a package, you must re-make LAMMPS.

Additional make options exist to help manage LAMMPS files that exist in both the src directory and in package sub-directories. Typing "make package-update" will overwrite src files with files from the package directories if the package has been included. Typing "make package-overwrite" will overwrite files in the package directories with src files. Typing "make package-check" will list differences between src and package versions of the same files.

To use the poems package you must build LAMMPS with the POEMS library, which computes the constrained rigid-body motion of articulated (jointed) multibody systems. POEMS was written and is distributed by Prof Kurt Anderson's group at Rensselaer Polytechnic Institute (RPI). It is included in the LAMMPS distribution. To build LAMMPS with POEMS, you must use a low-level LAMMPS Makefile that includes the POEMS directory in its paths. See Makefile.g++.poems as an example. You must also build POEMS itself as a library before building LAMMPS, so that LAMMPS can link against it. The POEMS library is built by typing "make" from within the poems directory in the LAMMPS distribution. By default

this uses Makefile which uses the gcc compiler. If you need to use another compiler (so that the POEMS library and LAMMPS are consistent), use another poems/Makefile.\* or create your own and invoke it as "make -f Makefile.\*".

### ***Building LAMMPS as a library:***

LAMMPS can be built as a library, which can then be called from another application or a scripting language. This is done by typing

```
make makelib
make -f Makefile.lib foo
```

where foo is the machine name. The first "make" command will create a current Makefile.lib with all the file names in your src dir. The 2nd "make" command will use it to build LAMMPS as a library. This requires that Makefile.foo have a library target (lib) and system-specific settings for ARCHIVE and ARFLAGS. See Makefile.linux for an example. This will create the file liblmp\_foo.a which another application can link to. The library has 3 callable functions:

```
void lammps_open(int, char **);
void lammps_close();
int lammps_command(char *);
```

The lammps\_open() function is used to initialize LAMMPS, passing in a list of strings as if they were command-line arguments when LAMMPS is run from the command line. The lammps\_close() function is used to shut down LAMMPS and free all its memory. The lammps\_command() function is used to pass a string to LAMMPS as if it were an input command read from an input script. See the library.cpp file for more information about the arguments and return values for these 3 functions.

### ***Additional build tips:***

(1) Building LAMMPS for multiple platforms.

You can make LAMMPS for multiple platforms from the same src directory. Each target creates its own object sub-dir called Obj\_name where it stores the system-specific \*.o files.

(2) Cleaning up.

Typing "make clean" will delete all \*.o object files created when LAMMPS is built.

(3) On some 64-bit machines, compiling with -O3 appears to break the Coulombic tabling option used by the pair\_style lj/cut/coul/long and lj/charmm/coul/long styles. By default, tabling is used by these styles since it can offer a 2x speed-up. It can be disabled via the pair\_modify command. Alternatively, the associated files (e.g. pair\_lj\_cut\_coul\_long.cpp) can be compiled with -O2, or with the compiler flag *-fno-strict-aliasing*. Either of those build changes seems to fix the problem.

(4) Building for a Macintosh.

OS X is BSD Unix, so it already works. See the Makefile.mac file.

(5) Building for MicroSoft Windows.

I've never done this, but LAMMPS is just standard C++ with MPI and FFT calls. You should be able to use cygwin to build LAMMPS with a Unix make. Or you should be able to pull all the source files into Visual C++ (ugh) or some similar development environment and build it. In the src/MAKE/Windows directory are some notes from users on how they built LAMMPS under Windows, so you can look at their instructions for tips. Good luck – I can't help you on this one.

---

## 2.3 Running LAMMPS

By default, LAMMPS runs by reading commands from stdin; e.g. `lmp_linux < in.file`. This means you first create an input script (e.g. `in.file`) containing the desired commands. [This section](#) describes how input scripts are structured and what commands they contain.

You can test LAMMPS on any of the sample inputs provided in the examples directory. Input scripts are named `in.*` and sample outputs are named `log.*.name.P` where `name` is a machine and `P` is the number of processors it was run on.

Here is how you might run one of the Lennard–Jones tests on a Linux box, using `mpirun` to launch a parallel job:

```
cd src
make linux
cp lmp_linux ../examples/lj
cd ../examples/lj
mpirun -np 4 lmp_linux <in.lj.nve
```

The screen output from LAMMPS is described in the next section. As it runs, LAMMPS also writes a `log.lammps` file with the same information. Note that this sequence of commands copied the LAMMPS executable (`lmp_linux`) to the directory with the input files. If you don't do this, LAMMPS may look for input files or create output files in the directory where the executable is, rather than where you run it from.

If LAMMPS encounters errors in the input script or while running a simulation it will print an ERROR message and stop or a WARNING message and continue. See [this section](#) for a discussion of the various kinds of errors LAMMPS can or can't detect, a list of all ERROR and WARNING messages, and what to do about them.

LAMMPS can run a problem on any number of processors, including a single processor. In theory you should get identical answers on any number of processors and on any machine. In practice, numerical round-off can cause slight differences and eventual divergence of molecular dynamics phase space trajectories.

LAMMPS can run as large a problem as will fit in the physical memory of one or more processors. If you run out of memory, you must run on more processors or setup a smaller problem.

---

## 2.4 Command-line options

At run time, LAMMPS recognizes several optional command-line switches which may be used in any order. For example, `lmp_ibm` might be launched as follows:

```
mpirun -np 16 lmp_ibm -var f tmp.out -log my.log -screen none <in.alloy
```

These are the command-line options:

```
-echo style
```

Set the style of command echoing. The style can be *none* or *screen* or *log* or *both*. Depending on the style, each command read from the input script will be echoed to the screen and/or logfile. This can be useful to figure out which line of your script is causing an input error. The default value is *log*. The echo style can also be set by using the echo command in the input script itself.

`-partition 8x2 4 5 ...`

Invoke LAMMPS in multi-partition mode. When LAMMPS is run on P processors and this switch is not used, LAMMPS runs in one partition, i.e. all P processors run a single simulation. If this switch is used, the P processors are split into separate partitions and each partition runs its own simulation. The arguments to the switch specify the number of processors in each partition. Arguments of the form MxN mean M partitions, each with N processors. Arguments of the form N mean a single partition with N processors. The sum of processors in all partitions must equal P. Thus the command "`-partition 8x2 4 5`" has 10 partitions and runs on a total of 25 processors.

The input script specifies what simulation is run on which partition; see the variable and next commands. Simulations running on different partitions can also communicate with each other; see the temper command.

`-in file`

Specify a file to use as an input script. This is an optional switch when running LAMMPS in one-partition mode. If it is not specified, LAMMPS reads its input script from stdin – e.g. `lmp_linux < in.run`. This is a required switch when running LAMMPS in multi-partition mode, since multiple processors cannot all read from stdin.

`-log file`

Specify a log file for LAMMPS to write status information to. In one-partition mode, if the switch is not used, LAMMPS writes to the file `log.lammps`. If this switch is used, LAMMPS writes to the specified file. In multi-partition mode, if the switch is not used, a `log.lammps` file is created with hi-level status information. Each partition also writes to a `log.lammps.N` file where N is the partition ID. If the switch is specified in multi-partition mode, the hi-level logfile is named "file" and each partition also logs information to a `file.N`. For both one-partition and multi-partition mode, if the specified file is "none", then no log files are created. Using a log command in the input script will override this setting.

`-screen file`

Specify a file for LAMMPS to write its screen information to. In one-partition mode, if the switch is not used, LAMMPS writes to the screen. If this switch is used, LAMMPS writes to the specified file instead and you will see no screen output. In multi-partition mode, if the switch is not used, hi-level status information is written to the screen. Each partition also writes to a `screen.N` file where N is the partition ID. If the switch is specified in multi-partition mode, the hi-level screen dump is named "file" and each partition also writes screen information to a `file.N`. For both one-partition and multi-partition mode, if the specified file is "none", then no screen output is performed.

`-var X value`

Specify a variable that will be defined for substitution purposes when the input script is read. X should be a single lower-case character from 'a' to 'z'. The value can be any string. Using this command-line option is equivalent to putting the line "variable X index value" at the beginning of the input script. See the variable command for more information.

---

## 2.5 LAMMPS screen output

As LAMMPS reads an input script, it prints information to both the screen and a log file about significant actions it takes to setup a simulation. When the simulation is ready to begin, LAMMPS performs various initializations and prints the amount of memory (in MBytes per processor) that the simulation requires. It also prints details of the initial thermodynamic state of the system. During the run itself, thermodynamic information is printed periodically, every few timesteps. When the run concludes, LAMMPS prints the final thermodynamic state and a total run time for the simulation. It then appends statistics about the CPU time and storage requirements for the simulation. An example set of statistics is shown here:

```
Loop time of 49.002 on 2 procs for 2004 atoms
```

```
Pair    time (%) = 35.0495 (71.5267)
Bond    time (%) = 0.092046 (0.187841)
Kspce   time (%) = 6.42073 (13.103)
Neigh   time (%) = 2.73485 (5.5811)
Comm    time (%) = 1.50291 (3.06703)
Outpt   time (%) = 0.013799 (0.0281601)
Other   time (%) = 2.13669 (4.36041)
```

```
Nlocal:    1002 ave, 1015 max, 989 min
Histogram: 1 0 0 0 0 0 0 0 0 1
Nghost:    8720 ave, 8724 max, 8716 min
Histogram: 1 0 0 0 0 0 0 0 0 1
Neighs:    354141 ave, 361422 max, 346860 min
Histogram: 1 0 0 0 0 0 0 0 0 1
```

```
Total # of neighbors = 708282
Ave neighs/atom = 353.434
Ave special neighs/atom = 2.34032
Number of reneighboring = 42
Dangerous reneighboring = 2
```

The first section gives the breakdown of the CPU run time (in seconds) into major categories. The second section lists the number of owned atoms (Nlocal), ghost atoms (Nghost), and pair-wise neighbors stored per processor. The max and min values give the spread of these values across processors with a 10-bin histogram showing the distribution. The total number of histogram counts is equal to the number of processors.

The last section gives aggregate statistics for pair-wise neighbors and special neighbors that LAMMPS keeps track of (see the special\_bonds command). The number of times neighbor lists were rebuilt during the run is given as well as the number of potentially "dangerous" rebuilds. If atom movement triggered neighbor list rebuilding (see the neigh\_modify command), then dangerous reneighboring is those that were triggered on the first timestep atom movement was checked for. If this count is non-zero you may wish to reduce the delay factor to insure no force interactions are missed by atoms moving beyond the neighbor skin distance before a rebuild takes place.

If an energy minimization was performed, additional information is printed that includes the energy change and convergence criteria.

---

## 2.6 Tips for users of previous LAMMPS versions

LAMMPS 2003 is a complete C++ rewrite of LAMMPS 2001, which was written in F90. Features of earlier versions of LAMMPS are listed in [this section](#). The F90 and F77 versions (2001 and 99) are also freely distributed as open-source codes; check the [LAMMPS WWW Site](#) for distribution information if you prefer those versions. The 99 and 2001 versions are no longer under active development; they do not have all the features of LAMMPS 2003.

If you are a previous user of LAMMPS 2001, these are the most significant changes you will notice in LAMMPS 2003:

- (1) The names and arguments of many input script commands have changed. All commands are now a single word (e.g. `read_data` instead of `read data`).
- (2) All the functionality of LAMMPS 2001 is included in LAMMPS 2003, but you may need to specify the relevant commands in different ways.
- (3) The format of the data file can be streamlined for some problems. See the [read\\_data](#) command for details. The data file section "Nonbond Coeff" has been renamed to "Pair Coeff" in LAMMPS 2003.
- (4) Binary restart files written by LAMMPS 2001 cannot be read by LAMMPS 2003 with a [read\\_restart](#) command. This is because they were output by F90 which writes in a different binary format than C or C++ writes or reads. Use the `restart2data` tool provided with LAMMPS 2001 to convert the 2001 restart file to a text data file. Then edit the data file as necessary before using the LAMMPS 2003 [read\\_data](#) command to read it in.
- (5) There are numerous small numerical changes in LAMMPS 2003 that mean you will not get identical answers when comparing to a 2001 run. However, your initial thermodynamic energy and MD trajectory should be close if you have setup the problem for both codes the same.

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---

## 3. Commands

This section describes how a LAMMPS input script is formatted and what commands are used to define a LAMMPS simulation.

- [3.1 LAMMPS input script](#)
  - [3.2 Parsing rules](#)
  - [3.3 Input script structure](#)
  - [3.4 Commands listed by category](#)
  - [3.5 Commands listed alphabetically](#)
- 

### 3.1 LAMMPS input script

LAMMPS executes by reading commands from an input script (text file), one line at a time. When the input script ends, LAMMPS exits. Each command causes LAMMPS to take some action. It may set an internal variable, read in a file, or run a simulation. Most commands have default settings, which means you only need

to use the command if you wish to change the default.

In many cases, the ordering of commands in an input script is not important. However the following rules apply:

(1) LAMMPS does not read your entire input script and then perform a simulation with all the settings. Rather, the input script is read one line at a time and each command takes effect when it is read. Thus this sequence of commands:

```
timestep 0.5
run      100
run      100
```

does something different than this sequence:

```
run      100
timestep 0.5
run      100
```

In the first case, the specified timestep (0.5 fmsec) is used for two simulations of 100 timesteps each. In the 2nd case, the default timestep (1.0 fmsec) is used for the 1st 100 step simulation and a 0.5 fmsec timestep is used for the 2nd one.

(2) Some commands are only valid when they follow other commands. For example you cannot set the temperature of a group of atoms until atoms have been defined and a group command is used to define which atoms belong to the group.

(3) Sometimes command B will use values that can be set by command A. This means command A must precede command B in the input script if it is to have the desired effect. For example, the read\_data command initializes the system by setting up the simulation box and assigning atoms to processors. If default values are not desired, the processors and boundary commands need to be used before read\_data to tell LAMMPS how to map processors to the simulation box.

Many input script errors are detected by LAMMPS and an ERROR or WARNING message is printed. This section gives more information on what errors mean. The documentation for each command lists restrictions on how the command can be used.

---

### 3.2 Parsing rules

Each non-blank line in the input script is treated as a command. LAMMPS commands are case sensitive. Command names are lower-case, as are specified command arguments. Upper case letters may be used in file names or user-chosen ID strings.

Here is how each line in the input script is parsed by LAMMPS:

(1) If the line ends with a `"` character (with no trailing whitespace), the command is assumed to continue on the next line. The next line is concatenated to the previous line by removing the `"` character and newline. This allows long commands to be continued across two or more lines.

(2) All characters from the first `#` character onward are treated as comment and discarded.

(3) The line is searched repeatedly for \$ characters. If the character following the \$ is "a" to "z", the two-character sequence (e.g. \$x) is replaced with the corresponding variable text. See the [variable](#) command for details.

(4) The line is broken into "words" separated by whitespace (tabs, spaces). Note that words can thus contain letters, digits, underscores, or punctuation characters.

(5) The first word is the command name. All successive words in the line are arguments.

(6) Text with spaces can be enclosed in double quotes so it will be treated as a single argument. See the [dump](#), [modify](#) or [fix print](#) commands for examples. A '#' or '\$' character in text between double quotes will also not be treated as a comment or substituted for as a variable.

---

### 3.3 Input script structure

This section describes the structure of a typical LAMMPS input script. The "examples" directory in the LAMMPS distribution contains many sample input scripts; the corresponding problems are discussed in [this section](#), and animated on the [LAMMPS WWW Site](#).

A LAMMPS input script typically has 4 parts:

1. Initialization
2. Atom definition
3. Settings
4. Run a simulation

The last 2 parts can be repeated as many times as desired. I.e. run a simulation, change some settings, run some more, etc. Each of the 4 parts is now described in more detail. Remember that almost all the commands need only be used if a non-default value is desired.

#### (1) Initialization

Set parameters that need to be defined before atoms are created or read-in from a file.

The relevant commands are [units](#), [dimension](#), [newton](#), [processors](#), [boundary](#), [atom\\_style](#), [atom\\_modify](#).

If force-field parameters appear in the files that will be read, these commands tell LAMMPS what kinds of force fields are being used: [pair\\_style](#), [bond\\_style](#), [angle\\_style](#), [dihedral\\_style](#), [improper\\_style](#).

#### (2) Atom definition

There are 3 ways to define atoms in LAMMPS. Read them in from a data or restart file via the [read\\_data](#) or [read\\_restart](#) commands. These files can contain molecular topology information. Or create atoms on a lattice (with no molecular topology), using these commands: [lattice](#), [orient](#), [origin](#), [region](#), [create\\_box](#), [create\\_atoms](#). The entire set of atoms can be duplicated to make a larger simulation using the [replicate](#) command.

#### (3) Settings

Once atoms and molecular topology are defined, a variety of settings can be specified: force field coefficients, simulation parameters, output options, etc.



Force field coefficients are set by these commands (they can also be set in the read-in files): pair coeff, bond coeff, angle coeff, dihedral coeff, improper coeff, kspace style, dielectric, special bonds.

Various simulation parameters are set by these commands: temperature, temp modify, neighbor, neigh modify, group, timestep, reset timestep, run style, min style, min modify.

Fixes impose a variety of boundary conditions, time integration, and diagnostic options. The fix command comes in many flavors.

Output options are set by these commands: thermo, dump, restart.

#### (4) Run a simulation

A molecular dynamics simulation is run using the run command. Energy minimization (molecular statics) is performed using the minimize command. A parallel tempering (replica-exchange) simulation can be run using the temper command.

---

### 3.4 Commands listed by category

This section lists all LAMMPS commands, grouped by category. The next section lists the same commands alphabetically. Note that some style options for some commands are part of specific LAMMPS packages, which means they cannot be used unless the package was included when LAMMPS was built. Not all packages are included in a default LAMMPS build. These dependencies are listed as Restrictions in the command's documentation.

Initialization:

atom modify, atom style, boundary, dimension, newton, processors, units

Atom definition:

create atoms, create box, lattice, orient, origin, read data, read restart, region, replicate

Force fields:

angle coeff, angle style, bond coeff, bond style, dielectric, dihedral coeff, dihedral style, improper coeff, improper style, kspace modify, kspace style, pair coeff, pair modify, pair style, pair write, special bonds

Settings:

dipole, group, mass, min modify, min style, neigh modify, neighbor, reset timestep, run style, set, temp modify, temperature, timestep, velocity

Fixes:

fix, fix modify, unfix

Output:

dump, dump modify, restart, thermo, thermo modify, thermo style, undump, write restart

Actions:

[delete atoms](#), [delete bonds](#), [displace atoms](#), [minimize](#), [run](#), [temper](#)

Miscellaneous:

[cd](#), [clear](#), [echo](#), [include](#), [jump](#), [label](#), [log](#), [next](#), [print](#), [variable](#)

---

### 3.5 Individual commands

This section lists all LAMMPS commands alphabetically. The [previous section](#) lists the same commands, grouped by category. Note that some style options for some commands are part of specific LAMMPS packages, which means they cannot be used unless the package was included when LAMMPS was built. Not all packages are included in a default LAMMPS build. These dependencies are listed as Restrictions in the command's documentation.

|                                |                                |                                |                                |                               |                               |
|--------------------------------|--------------------------------|--------------------------------|--------------------------------|-------------------------------|-------------------------------|
| <a href="#">angle coeff</a>    | <a href="#">angle style</a>    | <a href="#">atom modify</a>    | <a href="#">atom style</a>     | <a href="#">bond coeff</a>    | <a href="#">bond style</a>    |
| <a href="#">boundary</a>       | <a href="#">cd</a>             | <a href="#">clear</a>          | <a href="#">create atoms</a>   | <a href="#">create box</a>    | <a href="#">delete atoms</a>  |
| <a href="#">delete bonds</a>   | <a href="#">dielectric</a>     | <a href="#">dihedral coeff</a> | <a href="#">dihedral style</a> | <a href="#">dimension</a>     | <a href="#">dipole</a>        |
| <a href="#">displace atoms</a> | <a href="#">dump</a>           | <a href="#">dump modify</a>    | <a href="#">echo</a>           | <a href="#">fix</a>           | <a href="#">fix modify</a>    |
| <a href="#">group</a>          | <a href="#">improper coeff</a> | <a href="#">improper style</a> | <a href="#">include</a>        | <a href="#">jump</a>          | <a href="#">kspace modify</a> |
| <a href="#">kspace style</a>   | <a href="#">label</a>          | <a href="#">lattice</a>        | <a href="#">log</a>            | <a href="#">mass</a>          | <a href="#">minimize</a>      |
| <a href="#">min modify</a>     | <a href="#">min style</a>      | <a href="#">neigh modify</a>   | <a href="#">neighbor</a>       | <a href="#">newton</a>        | <a href="#">next</a>          |
| <a href="#">orient</a>         | <a href="#">origin</a>         | <a href="#">pair coeff</a>     | <a href="#">pair modify</a>    | <a href="#">pair style</a>    | <a href="#">pair write</a>    |
| <a href="#">print</a>          | <a href="#">processors</a>     | <a href="#">read data</a>      | <a href="#">read restart</a>   | <a href="#">region</a>        | <a href="#">replicate</a>     |
| <a href="#">reset timestep</a> | <a href="#">restart</a>        | <a href="#">run</a>            | <a href="#">run style</a>      | <a href="#">set</a>           | <a href="#">special bonds</a> |
| <a href="#">temp modify</a>    | <a href="#">temper</a>         | <a href="#">temperature</a>    | <a href="#">thermo</a>         | <a href="#">thermo modify</a> | <a href="#">thermo style</a>  |
| <a href="#">timestep</a>       | <a href="#">undump</a>         | <a href="#">unfix</a>          | <a href="#">units</a>          | <a href="#">variable</a>      | <a href="#">velocity</a>      |
| <a href="#">write restart</a>  |                                |                                |                                |                               |                               |

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## 4. How-to discussions

The following sections describe what commands can be used to perform certain kinds of LAMMPS simulations.

- 4.1 [Restarting a simulation](#)
- 4.2 [2d simulations](#)
- 4.3 [CHARMM and AMBER force fields](#)
- 4.4 [Running multiple simulations from one input script](#)
- 4.5 [Parallel tempering](#)
- 4.6 [Granular models](#)
- 4.7 [TIP3P water model](#)
- 4.8 [TIP4P water model](#)
- 4.9 [SPC water model](#)

The example input scripts included in the LAMMPS distribution and highlighted in [this section](#) also show how to setup and run various kinds of problems.

---

## 4.1 Restarting a simulation

There are 3 ways to continue a long LAMMPS simulation. Multiple [run](#) commands can be used in the same input script. Each run will continue from where the previous run left off. Or binary restart files can be saved to disk using the [restart](#) command. At a later time, these binary files can be read via a [read\\_restart](#) command in a new script. Or they can be converted to text data files and read by a [read\\_data](#) command in a new script. [This section](#) discusses the *restart2data* tool that is used to perform the conversion.

Here we give examples of 2 scripts that read either a binary restart file or a converted data file and then issue a new run command to continue where the previous run left off. They illustrate what settings must be made in the new script. Details are discussed in the documentation for the [read\\_restart](#) and [read\\_data](#) commands.

Look at the *in.chain* input script provided in the *bench* directory of the LAMMPS distribution to see the original script that these 2 scripts are based on. If that script had the line

```
restart          50 tmp.restart
```

added to it, it would produce 2 binary restart files (tmp.restart.50 and tmp.restart.100) as it ran.

This script could be used to read the 1st restart file and re-run the last 50 timesteps:

```
read_restart     tmp.restart.50

neighbor         0.4 bin
neigh_modify     every 1 delay 1

fix             1 all nve
fix             2 all langevin 1.0 1.0 10.0 904297

timestep        0.012

run             50
```

Note that the following commands do not need to be repeated because their settings are included in the restart file: *units*, *atom\_style*, *special\_bonds*, *pair\_style*, *bond\_style*. However these commands do need to be used, since their settings are not in the restart file: *neighbor*, *fix*, *timestep*.

If you actually use this script to perform a restarted run, you will notice that the thermodynamic data match at step 50 (if you also put a "thermo 50" command in the original script), but do not match at step 100. This is because the [fix langevin](#) command uses random numbers in a way that does not allow for perfect restarts.

As an alternate approach, the restart file could be converted to a data file using this tool:

```
restart2data tmp.restart.50 tmp.restart.data
```

Then, this script could be used to re-run the last 50 steps:

```
units           lj
atom_style      bond
```

```

pair_style      lj/cut 1.12
pair_modify     shift yes
bond_style      fene
special_bonds   0.0 1.0 1.0

read_data       tmp.restart.data

neighbor        0.4 bin
neigh_modify    every 1 delay 1

fix             1 all nve
fix             2 all langevin 1.0 1.0 10.0 904297

timestep        0.012

reset_timestep  50
run             50

```

Note that nearly all the settings specified in the original *in.chain* script must be repeated, except the *pair\_coeff* and *bond\_coeff* commands since the new data file lists the force field coefficients. Also, the reset timestep command is used to tell LAMMPS the current timestep. This value is stored in restart files, but not in data files.

---

## 4.2 2d simulations

Use the dimension command to specify a 2d simulation.

Make the simulation box periodic in z via the boundary command. This is the default.

If using the create box command to define a simulation box, set the z dimensions narrow, but finite, so that the create\_atoms command will tile the 3d simulation box with a single z plane of atoms – e.g.

```
create_box 1 -10 10 -10 10 -0.25 0.25
```

If using the read data command to read in a file of atom coordinates, set the "zlo zhi" values to be finite but narrow, similar to the create\_box command settings just described. For each atom in the file, assign a z coordinate so it falls inside the z-boundaries of the box – e.g. 0.0.

Use the fix enforce2d command as the last defined fix to insure that the z-components of velocities and forces are zeroed out every timestep. The reason to make it the last fix is so that any forces induced by other fixes will be zeroed out.

Many of the example input scripts included in the LAMMPS distribution are for 2d models.

---

## 4.3 CHARMM and AMBER force fields

There are many different ways to compute forces in the CHARMM and AMBER molecular dynamics codes, only some of which are available as options in LAMMPS. A force field has 2 parts: the formulas that define it and the coefficients used for a particular system. Here we only discuss formulas implemented in LAMMPS. Setting coefficients is done in the input data file via the read data command or in the input script with commands like pair coeff or bond coeff. See this section for additional tools that can use CHARMM or

AMBER to assign force field coefficients and convert their output into LAMMPS input.

These style choices compute force field formulas that are consistent with common options in CHARMM or AMBER. See each command's documentation for the formula it computes.

- bond\_style harmonic
  - angle\_style charmm
  - dihedral\_style charmm
  - pair\_style lj/charmm/coul/charmm
  - pair\_style lj/charmm/coul/charmm/implicit
  - pair\_style lj/charmm/coul/long
  
  - special\_bonds charmm
  - special\_bonds amber
- 

#### 4.4 Running multiple simulations from one input script

This can be done in several ways. See the documentation for individual commands for more details on how these examples work.

If "multiple simulations" means continue a previous simulation for more timesteps, then you simply use the run command multiple times. For example, this script

```
units lj
atom_style atomic
read_data data.lj
run 10000
run 10000
run 10000
run 10000
run 10000
```

would run 5 successive simulations of the same system for a total of 50,000 timesteps.

If you wish to run totally different simulations, one after the other, the clear command can be used in between them to re-initialize LAMMPS. For example, this script

```
units lj
atom_style atomic
read_data data.lj
run 10000
clear
units lj
atom_style atomic
read_data data.lj.new
run 10000
```

would run 2 independent simulations, one after the other.

For large numbers of independent simulations, you can use variables and the next and jump commands to loop over the same input script multiple times with different settings. For example, this script, named in.polymer

```

variable d index run1 run2 run3 run4 run5 run6 run7 run8
cd $d
read_data data.polymer
run 10000
cd ..
clear
next d
jump in.polymer

```

would run 8 simulations in different directories, using a data.polymer file in each directory. The same concept could be used to run the same system at 8 different temperatures, using a temperature variable and storing the output in different log and dump files, for example

```

variable a loop 8
variable t index 0.8 0.85 0.9 0.95 1.0 1.05 1.1 1.15
log log.$a
read data.polymer
velocity all create $t 352839
fix 1 all nvt $t $t 100.0
dump 1 all atom 1000 dump.$a
run 100000
next t
next a
jump in.polymer

```

All of the above examples work whether you are running on 1 or multiple processors, but assumed you are running LAMMPS on a single partition of processors. LAMMPS can be run on multiple partitions via the "-partition" command-line switch as described in [this section](#) of the manual.

In the last 2 examples, if LAMMPS were run on 3 partitions, the same scripts could be used if the "index" and "loop" variables were replaced with *universe*-style variables, as described in the [variable](#) command. Also, the "next t" and "next a" commands would need to be replaced with a single "next a t" command. With these modifications, the 8 simulations of each script would run on the 3 partitions one after the other until all were finished. Initially, 3 simulations would be started simultaneously, one on each partition. When one finished, that partition would then start the 4th simulation, and so forth, until all 8 were completed.

---

## 4.5 Parallel tempering

The [temper](#) command can be used to perform a parallel tempering or replica-exchange simulation where multiple copies of a simulation are run at different temperatures on different sets of processors, and Monte Carlo temperature swaps are performed between pairs of copies.

Use the `-procs` and `-in` [command-line switches](#) to launch LAMMPS on multiple partitions.

In your input script, define a set of temperatures, one for each processor partition, using the [variable](#) command:

```
variable t proc 300.0 310.0 320.0 330.0
```

Define a fix of style [nvt](#) or [langevin](#) to control the temperature of each simulation:

```
fix myfix all nvt $t $t 100.0
```

Use the temper command in place of a run command to perform a simulation where tempering exchanges will take place:

```
temper 100000 100 $t myfix 3847 58382
```

---

## 4.6 Granular models

To run a simulation of a granular model, you will want to use the following commands:

- atom\_style granular
- fix nve/gran
- fix gravity
- thermo\_style gran

Use one of these 3 pair potentials:

- pair\_style gran/history
- pair\_style gran/no\_history
- pair\_style gran/hertzian

These commands implement fix options specific to granular systems:

- fix freeze
- fix gran/diag
- fix insert
- fix viscous
- fix wall/gran

The fix style *freeze* zeroes both the force and torque of frozen atoms, and should be used for granular system instead of the fix style *setforce*.

For computational efficiency, you can eliminate needless pairwise computations between frozen atoms by using this command:

- neigh\_modify exclude
- 

## 4.7 TIP3P water model

The TIP3P water model as implemented in CHARMM (MacKerell) specifies a 3-site rigid water molecule with charges and Lennard–Jones parameters assigned to each of the 3 atoms. In LAMMPS the fix shake command can be used to hold the two O–H bonds and the H–O–H angle rigid. A bond style of *harmonic* and an angle style of *harmonic* or *charmm* should also be used.

These are the additional parameters (in real units) to set for O and H atoms and the water molecule to run a rigid TIP3P–CHARMM model with a cutoff. The K values can be used if a flexible TIP3P model (without fix shake) is desired. If the LJ epsilon and sigma for HH and OH are set to 0.0, it corresponds to the original 1983 TIP3P model (Jorgensen).

O mass = 15.9994  
H mass = 1.008

O charge = -0.834  
H charge = 0.417

LJ epsilon of OO = 0.1521  
LJ sigma of OO = 3.1507  
LJ epsilon of HH = 0.0460  
LJ sigma of HH = 0.4000  
LJ epsilon of OH = 0.0836  
LJ sigma of OH = 1.7753

K of OH bond = 450  
r0 of OH bond = 0.9572

K of HOH angle = 55  
theta of HOH angle = 104.52

These are the parameters to use for TIP3P with a long-range Coulombic solver (Ewald or PPPM in LAMMPS):

O mass = 15.9994  
H mass = 1.008

O charge = -0.830  
H charge = 0.415

LJ epsilon of OO = 0.102  
LJ sigma of OO = 3.1507  
LJ epsilon, sigma of OH, HH = 0.0

K of OH bond = 450  
r0 of OH bond = 0.9572

K of HOH angle = 55  
theta of HOH angle = 104.52

---

#### 4.8 TIP4P water model

The four-point TIP4P rigid water model extends the traditional three-point TIP3P model by adding an additional site, usually massless, where the charge associated with the oxygen atom is placed. This site M is located at a fixed distance away from the oxygen along the bisector of the HOH bond angle. A bond style of *harmonic* and an angle style of *harmonic* or *charmm* should also be used.

Two different four-point models (cutoff and long-range Coulombics) can be implemented using LAMMPS pair styles with *tip4p* in their style name. For both models, the bond lengths and bond angles should be held fixed using the [fix shake](#) command.



These are the additional parameters (in real units) to set for O and H atoms and the water molecule to run a rigid TIP4P model with a cutoff (Jorgensen). Note that the OM distance is specified in the pair\_style command, not as part of the pair coefficients.

O mass = 15.9994

H mass = 1.008

O charge = -1.040

H charge = 0.520

r0 of OH bond = 0.9572

theta of HOH angle = 104.52

OM distance = 0.15

LJ epsilon of O-O = 0.1550

LJ sigma of O-O = 3.1536

LJ epsilon, sigma of OH, HH = 0.0

These are the parameters to use for TIP4P with a long-range Coulombic solver (Ewald or PPPM in LAMMPS):

O mass = 15.9994

H mass = 1.008

O charge = -1.0484

H charge = 0.5242

r0 of OH bond = 0.9572

theta of HOH angle = 104.52

OM distance = 0.1250

LJ epsilon of O-O = 0.16275

LJ sigma of O-O = 3.16435

LJ epsilon, sigma of OH, HH = 0.0

---

#### 4.9 SPC water model

The SPC water model specifies a 3-site rigid water molecule with charges and Lennard-Jones parameters assigned to each of the 3 atoms. In LAMMPS the fix shake command can be used to hold the two O-H bonds and the H-O-H angle rigid. A bond style of *harmonic* and an angle style of *harmonic* or *charmm* should also be used.

These are the additional parameters (in real units) to set for O and H atoms and the water molecule to run a rigid SPC model with long-range Coulombics (Ewald or PPPM in LAMMPS).

O mass = 15.9994

H mass = 1.008

O charge = -0.820

H charge = 0.410

LJ epsilon of OO = 0.1553

LJ sigma of OO = 3.166

LJ epsilon, sigma of OH, HH = 0.0

r0 of OH bond = 1.0

theta of HOH angle = 109.47

---

**(Horn)** Horn, Swope, Pitner, Madura, Dick, Hura, and Head-Gordon, J Chem Phys, 120, 9665 (2004).

**(MacKerell)** MacKerell, Bashford, Bellott, Dunbrack, Evanseck, Field, Fischer, Gao, Guo, Ha, et al, J Phys Chem, 102, 3586 (1998).

**(Jorgensen)** Jorgensen, Chandrasekhar, Madura, Impey, Klein, J Chem Phys, 79, 926 (1983).

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## 5. Example problems

The LAMMPS distribution includes an examples sub-directory with several sample problems. Each problem is in a sub-directory of its own. Most are 2d models so that they run quickly, requiring at most a couple of minutes to run on a desktop machine. Each problem has an input script (in.\*) and produces a log file (log.\*) and dump file (dump.\*) when it runs. Some use a data file (data.\*) of initial coordinates as additional input. A few sample log file outputs on different machines and different numbers of processors are included in the directories to compare your answers to. E.g. a log file like log.crack.foo.P means it ran on P processors of machine "foo".

The dump files produced by the example runs can be animated using the xmovie tool described in the [Tools section](#). MPEG versions of most of the xmovie animations are also viewable from the Examples page of the [LAMMPS WWW Site](#).

These are the sample problems in the examples sub-directories:

|          |   |
|----------|---|
| crack    | crack propagation in a 2d solid             |
| flow     | Couette and Poiseuille flow in a 2d channel |
| friction | frictional contact of spherical             |

|          |  |
|----------|--|
|          | asperities<br>between 2d<br>surfaces                                     |
| indent   | spherical<br>indenter into a<br>2d solid                                 |
| melt     | rapid melt of<br>3d LJ system  |
| micelle  | self-assembly<br>of small<br>lipid-like<br>molecules into<br>2d bilayers |
| min      | energy<br>minimization<br>of 2d LJ melt                                  |
| obstacle | flow around<br>two voids in a<br>2d channel                              |
| peptide  | dynamics of a<br>small solvated<br>peptide chain<br>(5-mer)              |
| pour     | pouring of<br>granular<br>particles into a<br>3d box, then<br>chute flow |
| rigid    | rigid bodies<br>modeled as<br>independent or<br>coupled                  |
| shear    | sideways shear<br>applied to 2d<br>solid, with and<br>without a void     |

Here is how you might run and visualize one of the sample problems:

```
cd indent
cp ../../src/lmp_linux .           # copy LAMMPS executable to this dir
lmp_linux <in.indent                # run the problem
```

Running the simulation produces the files *dump.indent* and *log.lammps*. You can visualize the dump file as follows:

```
../../tools/xmovie/xmovie -scale dump.indent
```

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## 6. Performance & scalability

LAMMPS performance on several prototypical benchmarks and machines is discussed on the Benchmarks page of the [LAMMPS WWW Site](#) where CPU timings and parallel efficiencies are listed. Here, the benchmarks are described briefly and some useful rules of thumb about their performance are highlighted.

These are the 5 benchmark problems:

1. LJ = atomic fluid, Lennard–Jones potential with 2.5 sigma cutoff (55 neighbors per atom), NVE integration
2. Chain = bead–spring polymer melt of 100–mer chains, FENE bonds and LJ pairwise interactions with a  $2^{1/6}$  sigma cutoff (5 neighbors per atom), NVE integration
3. EAM = metallic solid, Cu EAM potential with 4.95 Angstrom cutoff (45 neighbors per atom), NVE integration
4. Chute = granular chute flow, frictional history potential with 1.1 sigma cutoff (7 neighbors per atom), NVE integration
5. Rhodo = rhodopsin protein in solvated lipid bilayer, CHARMM force field with a 10 Angstrom LJ cutoff (440 neighbors per atom), particle–particle particle–mesh (PPPM) for long–range Coulombics, NPT integration

The input files for running the benchmarks are included in the LAMMPS distribution, as are sample output files. Each of the 5 problems has 32,000 atoms and runs for 100 timesteps. Each can be run as a serial benchmarks (on one processor) or in parallel. In parallel, each benchmark can be run as a fixed–size or scaled–size problem. For fixed–size benchmarking, the same 32K atom problem is run on various numbers of processors. For scaled–size benchmarking, the model size is increased with the number of processors. E.g. on 8 processors, a 256K–atom problem is run; on 1024 processors, a 32–million atom problem is run, etc.

A useful metric from the benchmarks is the CPU cost per atom per timestep. Since LAMMPS performance scales roughly linearly with problem size and timesteps, the run time of any problem using the same model (atom style, force field, cutoff, etc) can then be estimated. For example, on a 1.7 GHz Pentium desktop machine (Intel icc compiler under Red Hat Linux), the CPU run–time in seconds/atom/timestep for the 5 problems is

| Problem:       | LJ      | Chain   | EAM     | Chute   | Rhodopsin |
|----------------|---------|---------|---------|---------|-----------|
| CPU/atom/step: | 4.55E–6 | 2.18E–6 | 9.38E–6 | 2.18E–6 | 1.11E–4   |
| Ratio to LJ:   | 1.0     | 0.48    | 2.06    | 0.48    | 24.5      |

The ratios mean that if the atomic LJ system has a normalized cost of 1.0, the bead–spring chains and granular systems run 2x faster, while the EAM metal and solvated protein models run 2x and 25x slower respectively. The bulk of these cost differences is due to the expense of computing a particular pairwise force field for a given number of neighbors per atom.

Performance on a parallel machine can also be predicted from the one–processor timings if the parallel efficiency can be estimated. The communication bandwidth and latency of a particular parallel machine affects the efficiency. On most machines LAMMPS will give fixed–size parallel efficiencies on these benchmarks above 50% so long as the atoms/processor count is a few 100 or greater – i.e. on 64 to 128 processors. Likewise, scaled–size parallel efficiencies will typically be 80% or greater up to very large processor counts. The benchmark data on the [LAMMPS WWW Site](#) gives specific examples on some different machines, including a run of 3/4 of a billion LJ atoms on 1500 processors that ran at 85% parallel efficiency.

## 7. Additional tools

LAMMPS is designed to be a computational kernel for performing molecular dynamics computations. Additional pre- and post-processing steps are often necessary to setup and analyze a simulation. A few additional tools are provided with the LAMMPS distribution and are described in this section.

Our group has also written and released a separate toolkit called [Pizza.py](#) which provides tools for doing setup, analysis, plotting, and visualization for LAMMPS simulations. Pizza.py is written in [Python](#) and is available for download from [the Pizza.py WWW site](#).

Note that many users write their own setup or analysis tools or use other existing codes and convert their output to a LAMMPS input format or vice versa. The tools listed here are included in the LAMMPS distribution as examples of auxiliary tools. Some of them are not actively supported by Sandia, as they were contributed by LAMMPS users. If you have problems using them, we can direct you to the authors.

The source code for each of these codes is in the tools sub-directory of the LAMMPS distribution. There is a Makefile (which you may need to edit for your platform) which will build several of the tools which reside in that directory. Some of them are larger packages in their own sub-directories with their own Makefiles.

- [replicate](#)
- [restart2data](#)
- [binary2txt](#)
- [data2xmovie](#)
- [chain](#)
- [micelle2d](#)
- [xmovie](#)
- [ch2lmp](#)
- [msi2lmp](#)
- [amber2lammmps](#)
- [lmp2arc](#)
- [lmp2cfg](#)
- [lmp2traj](#)

---

### replicate tool

The file replicate.c takes a LAMMPS data file and replicates it into a larger system. The syntax for running the tool is

```
replicate options <infile > outfile
```

See the top of the replicate.c file for a discussion of the options. This tool is used by some of the [LAMMPS benchmarks](#) for creating larger systems to run scaled-size problems on multiple processors.

---

## restart2data tool

The file `restart2data.cpp` converts a binary LAMMPS restart file into an ASCII data file. The syntax for running the tool is

```
restart2data restart-file data-file
```

This tool must be compiled on a platform that can read the binary file created by a LAMMPS run, since binary files are not compatible across all platforms.

Note that a text data file has less precision than a binary restart file. Hence, continuing a run from a converted data file will typically not conform as closely to a previous run as will restarting from a binary restart file.

---

## binary2txt tool

The file `binary2txt.cpp` converts one or more binary LAMMPS dump file into ASCII text files. The syntax for running the tool is

```
binary2txt file1 file2 ...
```

which creates `file1.txt`, `file2.txt`, etc. This tool must be compiled on a platform that can read the binary file created by a LAMMPS run, since binary files are not compatible across all platforms.

---

## data2xmovie tool

The file `data2xmovie.c` converts a LAMMPS data file into a snapshot suitable for visualizing with the [xmovie](#) tool, as if it had been output with a `dump` command from LAMMPS itself. The syntax for running the tool is

```
data2xmovie options <infile > outfile
```

See the top of the `data2xmovie.c` file for a discussion of the options.

---

## chain tool

The file `chain.f` creates a LAMMPS data file containing bead-spring polymer chains and/or monomer solvent atoms. It uses a text file containing chain definition parameters as an input. The created chains and solvent atoms can strongly overlap, so LAMMPS needs to run the system initially with a "soft" pair potential to un-overlap it. The syntax for running the tool is

```
chain <def.chain > data.file
```

See the `def.chain` or `def.chain.ab` files in the tools directory for examples of definition files. This tool was used to create the system for the [chain benchmark](#).

---

## micelle2d tool

The file `micelle2d.f` creates a LAMMPS data file containing short lipid chains in a monomer solution. It uses a text file containing lipid definition parameters as an input. The created molecules and solvent atoms can strongly overlap, so LAMMPS needs to run the system initially with a "soft" pair potential to un-overlap it. The syntax for running the tool is

```
micelle2d <def.micelle2d > data.file
```

See the def.micelle2d file in the tools directory for an example of a definition file. This tool was used to create the system for the [micelle example](#).

---

## **xmovie tool**

The xmovie tool is an X-based visualization package that can read LAMMPS dump files and animate them. It is in its own sub-directory with the tools directory. You may need to modify its Makefile so that it can find the appropriate X libraries to link against.

The syntax for running xmovie is

```
xmovie options dump.file1 dump.file2 ...
```

If you just type "xmovie" you will see a list of options. Note that by default, LAMMPS dump files are in scaled coordinates, so you typically need to use the `-scale` option with xmovie. When xmovie runs it opens a visualization window and a control window. The control options are straightforward to use.

Xmovie was mostly written by Mike Uttormark (U Wisconsin) while he spent a summer at Sandia. It displays 2d projections of a 3d domain. While simple in design, it is an amazingly fast program that can render large numbers of atoms very quickly. It's a useful tool for debugging LAMMPS input and output and making sure your simulation is doing what you think it should. The animations on the Examples page of the [LAMMPS WWW site](#) were created with xmovie.

I've lost contact with Mike, so I hope he's comfortable with us distributing his great tool!

---

## **ch2lmp tool**

The ch2lmp sub-directory contains tools for converting files back-and-forth between the CHARMM MD code and LAMMPS.

They are intended to make it easy to use CHARMM as a builder and as a post-processor for LAMMPS. Using `charmm2lammps.pl`, you can convert an ensemble built in CHARMM into its LAMMPS equivalent. Using `lammps2pdb.pl` you can convert LAMMPS atom dumps into pdb files.

See the README file in the ch2lmp sub-directory for more information.

These tools were created by Pieter in't Veld ([pjintve@sandia.gov](mailto:pjintve@sandia.gov)) and Paul Crozier ([pscrozi@sandia.gov](mailto:pscrozi@sandia.gov)) at Sandia.

---

## **msi2lmp tool**

The msi2lmp sub-directory contains a tool for creating LAMMPS input data files from Accelrys's Insight MD code (formerly MSI/Biosym and its Discover MD code). See the README file for more information.

This tool was written by John Carpenter (Cray), Michael Peachey (Cray), and Steve Lustig (Dupont). John is now at the Mayo Clinic ([jec@mayo.edu](mailto:jec@mayo.edu)), but still fields questions about the tool.

This tool may be out-of-date with respect to the current LAMMPS and Insight versions. Since we don't use it at Sandia, you'll need to experiment with it yourself.

---

## amber2Imp tool

The amber2Imp sub-directory contain two Python scripts for converting files back-and-forth between the AMBER MD code and LAMMPS. See the README file in amber2Imp for more information.

These tools were written by Keir Novik while he was at Queen Mary University of London. Keir is no longer there and cannot support these tools which are out-of-date with respect to the current LAMMPS version (and maybe with respect to AMBER as well). Since we don't use these tools at Sandia, you'll need to experiment with them and make necessary modifications yourself.

---

## Imp2arc tool

The Imp2arc sub-directory contains a tool for converting LAMMPS output files to the format for Accelrys's Insight MD code (formerly MSI/Biosysm and its Discover MD code). See the README file for more information.

This tool was written by John Carpenter (Cray), Michael Peachey (Cray), and Steve Lustig (Dupont). John is now at the Mayo Clinic ([jec@mayo.edu](mailto:jec@mayo.edu)), but still fields questions about the tool.

This tool was updated for the current LAMMPS C++ version by Jeff Greathouse at Sandia ([jagreat@sandia.gov](mailto:jagreat@sandia.gov)).

---

## Imp2cfg tool

The Imp2cfg sub-directory contains a tool for converting LAMMPS output files into a series of \*.cfg files which can be read into the AtomEye visualizer. See the README file for more information.

This tool was written by Ara Kooser at Sandia ([askoose@sandia.gov](mailto:askoose@sandia.gov)).

---

## Imp2traj tool

The Imp2traj sub-directory contains a tool for converting LAMMPS output files into 3 analysis files. One file can be used to create contour maps of the atom positions over the course of the simulation. The other two files provide density profiles and dipole moments. See the README file for more information.

This tool was written by Ara Kooser at Sandia ([askoose@sandia.gov](mailto:askoose@sandia.gov)).

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---

## 8. Modifying & extending LAMMPS

LAMMPS is designed in a modular fashion so as to be easy to modify and extend with new functionality. In this section, changes and additions users can make are listed along with some minimal instructions. Realistically, the best way to add a new feature is to find a similar feature in LAMMPS and look at the corresponding source and header files to figure out what it does. You will need some knowledge of C++ to be able to understand the hi-level structure of LAMMPS and its class organization, but functions (class methods) that do actual computations are written in vanilla C-style code and operate on simple C-style data structures (vectors and arrays).



Most of the new features described in this section require you to write a new C++ class (except for dump, thermo, and variable options, described below, where you can make small edits to existing files). Creating a new class requires 2 files, a source code file (\*.cpp) and a header file (\*.h). Their contents are briefly discussed below. Enabling LAMMPS to invoke the new class is as simple as adding two definition lines to the style\_user.h file, in the same syntax as the existing LAMMPS classes are defined in the style.h file.

The power of C++ and its object-orientation is that usually, all the code and variables needed to define the new feature are contained in the 2 files you write, and thus shouldn't make the rest of the code more complex or cause side-effect bugs.

Here is a concrete example. Suppose you write 2 files pair\_foo.cpp and pair\_foo.h that define a new class PairFoo that computes pairwise potentials described in the classic 1997 [paper](#) by Foo, et. al. If you wish to invoke those potentials in a LAMMPS input script with a command like

```
pair_style foo 0.1 3.5
```

you simply need to put your 2 files in the LAMMPS src directory, add 2 lines to the style\_user.h file, and re-make the code.

The first line added to style\_user.h would be

```
PairStyle(foo,PairFoo)
```

in the #ifdef PairClass section, where "foo" is the style keyword in the pair\_style command, and PairFoo is the class name in your C++ files.

The 2nd line added to style\_user.h would be

```
#include "pair_foo.h"
```

in the #ifdef PairInclude section, where pair\_foo.h is the name of your new include file.

When you re-make LAMMPS, your new pairwise potential becomes part of the executable and can be invoked with a pair\_style command like the example above. Arguments like 0.1 and 3.5 can be defined and processed by your new class.

Note that if you are using Makefile.list instead of Makefile to build LAMMPS, you will need to explicitly add the names of your new .cpp and .h file to Makefile.list.

Here is a list of the kinds of new features that can be added in this way. The dump and thermo options do not typically require new styles; LAMMPS can simply be recompiled after new code is added to dump\_custom.cpp or thermo\_custom.cpp.

- [Pairwise potentials](#)
- [Bond, angle, dihedral, improper potentials](#)
- [Dump options](#)
- [Thermodynamic output options](#)
- [Temperature computation options](#)
- [Region geometry options](#)
- [Fix options](#) which include integrators, temperature and pressure control, force constraints, boundary conditions, diagnostic output, etc

- Atom options
- Variable options
- New top-level commands

As illustrated by the pairwise example, these options are referred to in the LAMMPS documentation as the "style" of a particular command.

The instructions below for each category will list the header file for the parent class that these styles are sub-classes of. Public variables in that file are ones used and set by the sub-classes which are also used by the parent class. Sometimes they are also used by the rest of LAMMPS. Virtual functions in the header file which are set = 0 are ones you must define in your new class to give it the functionality LAMMPS expects. Virtual functions that are not set to 0 are functions you can optionally define.

Here are some additional guidelines for modifying LAMMPS and adding new functionality:

Think about whether what you want to do would be better as a pre- or post-processing step. Many computations are more easily and more quickly done that way.

Don't do anything within the timestepping of a run that isn't parallel. E.g. don't accumulate a bunch of data on a single processor and analyze it. You run the risk of seriously degrading the parallel efficiency.

If your new feature reads arguments or writes output, make sure you follow the unit conventions discussed by the units command.

If you add something you think is truly useful and doesn't impact LAMMPS performance when it isn't used, send me an email. We might be interested in adding it to the LAMMPS distribution.

---

## Pairwise potentials

All classes that compute pairwise interactions are sub-classes of the Pair class. See the pair.h file for a list of methods this class defines.

Pair\_lj\_cut.cpp and pair\_lj\_cut.h are the simplest example of a Pair class. They implement the *lj/cut* style of the pair\_style command.

Here is a brief description of the class methods in pair.h:

|          |  |
|----------|--|
| compute  | the<br>workhorse<br>routine that<br>computes the<br>pairwise<br>interactions |
| settings | reads the<br>input script<br>line with any<br>arguments<br>you define        |
| coeff    |  |

|                              |   |
|------------------------------|---|
|                              | set coefficients for one i,j type pair                            |
| init_one                     | perform initialization for one i,j type pair                      |
| write &read_restart          | write/read i,j pair coeffs to restart files                       |
| write &read_restart_settings | write/read global settings to restart files                       |
| single                       | force and energy of a single pairwise interaction between 2 atoms |
| compute_inner/middle/outer   | versions of compute used by rRESPA                                |

The inner/middle/outer routines are optional. Only a few of the pairwise potentials use these in conjunction with rRESPA as set by the run\_style command.

---

## Bond, angle, dihedral, improper potentials

All classes that compute molecular interactions are sub-classes of the Bond, Angle, Dihedral, and Improper classes. See the bond.h, angle.h, dihedral.h, and improper.h file for a list of methods these classes defines.

Bond\_harmonic.cpp and bond\_harmonic.h are the simplest example of a Bond class. Ditto for the harmonic forms of the angle, dihedral, and improper style commands. The bond\_harmonic files implement the *harmonic* style of the bond\_style command.

Here is a brief description of the class methods in bond.h, angle.h, etc:

|         |  |
|---------|--|
| compute | the workhorse routine that computes the molecular interactions |
| coeff   |  |

|                      |   |
|----------------------|---|
|                      | set<br>coefficients<br>for one bond<br>type |
| equilibrium_distance | length of<br>bond, used<br>by SHAKE         |
| write & read_restart | writes/reads<br>coeffs to<br>restart files  |
| single               | force and<br>energy of a<br>single bond     |

---

## Dump options

There are several classes that print dump files (snapshots of atoms) that are sub-classes of the Dump class. These include the dump\_atom.cpp, dump\_bond.cpp, and dump\_custom.cpp files.

New dump classes can be added, but it is typically simpler to modify the DumpCustom class contained in the dump\_custom.cpp file. See the dump command and its *custom* style for a list of what atom information can already be dumped by DumpCustom. If the attribute you want to dump is not in the list, or if you define a new atom style with new attributes (e.g. atoms that store their own magnetic moment), here is how to dump it out in a snapshot file:

Search the dump\_custom.cpp and dump\_custom.h files for the word "customize". It appears in roughly half a dozen locations. In each of the locations you can add a bit of code that will extend the DumpCustom class to enable it to dump a new quantity. E.g. you will add a keyword, add an if test, add a new small method that packs the requested data into a buffer, etc. For the latter, you can perform a modest amount of computation in this method; see the pack\_xs() function for an example.

If desired, a dump custom option can also compute more complicated quantities by invoking a fix that computed quantities at the end of a timestep (should be the same timestep the dump is invoked on). See the ENERGY, CENTRO, and stress options (SXX, SYY, etc) in dump\_custom.cpp for examples.

When you re-make LAMMPS, your new option should now be useable via the dump custom command.

---

## Thermodynamic output options

There is only one class that computes and prints thermodynamic information to the screen and log file, although the thermo style command treats its options as styles.

There are several styles defined in thermo.cpp: "one", "multi", and "granular". There is also a flexible "custom" style which allows you to specify what quantities will be printed each timestep where thermodynamics is computed. See the thermo style command for a list of pre-defined quantities.

Here is how you can extend the thermo output capabilities. Search the thermo.cpp and thermo.h files for the word "customize" which will tell you where to make these additions. Note that fixes can also print-out

thermodynamic quantities via the fix\_modify command, so you do not need to modify thermo.cpp to print fix information.

If you want to create a new style (like "one" or "granular") that prints a collection of pre-defined quantities, you add a few lines that define the new style to thermo.cpp. First, add a #DEFINE line at the top of the file which lists the quantities to print. Then add the style name you have chosen to the if test in the constructor to copy the defined string to the line variable.

You can also add new quantities to the custom list. Add your new keyword to the if test in the parse\_fields() function where the call to addfield() specifies the text string (8 character max) that will be printed with the quantity, the function that will compute it, and the data type (INT,FLOAT) of the quantity. Then at the bottom of the file, add a function compute\_\*() which computes the quantity you wish to print. The function assigns the quantity to the variable "dvalue" if it is a floating-point quantity, or to "ivalue" if it is an integer. See the other compute\_\*() functions for examples of how various quantities can be accessed, computed, summed across processors, normalized as per-atom values, etc. Also, if it makes sense to allow the quantity to be stored in a variable in the input script, add a couple of lines to the compute\_value() function that is called when a variable is evaluated. Finally, add a prototype for your new compute method to thermo.h.

---

## Temperature computation options

All classes that compute the temperature of the system are sub-classes of the Temperature class. See the temperature.h file for a list of methods these classes defines. Temperatures are computed by LAMMPS when velocities are set, when thermodynamics are computed, and when temperature is controlled by various thermostats like the fix nvt or fix langevin commands.

Temp\_full.cpp and temp\_full.h are the simplest example of a Temperature class. They implement the *full* style of the temperature command.

Here is a brief description of the class methods in temperature.h:

|         |                                   |
|---------|-----------------------------------|
| init    | setup the temperature computation |
| compute | compute and return temperature    |

---

## Region geometry options

All classes that define geometric regions are sub-classes of the Region class. See the region.h file for a list of methods these classes defines. Regions are used elsewhere in LAMMPS to group atoms, delete atoms to create a void, insert atoms in a specified region, etc.

Region\_sphere.cpp and region\_sphere.h are the simplest example of a Region class. They implement the *sphere* style of the region command.

Here is a brief description of the single class method required:

|       |  |
|-------|--|
| match | determine whether a point is in the region |
|-------|--|

---

## Fix options

In LAMMPS, a "fix" is any operation that is computed during timestepping that alters some property of the system. Essentially everything that happens during a simulation besides force computation, neighbor list manipulation, and output, is a "fix". This includes time integration (update of velocity and coordinates), force constraints (SHAKE or walls), and diagnostics (compute a diffusion coefficient). See the `fix.h` file for a list of methods these classes defines.

There are dozens of fix options in LAMMPS; choose one as a template that is similar to what you want to implement. They can be as simple as zeroing out forces (see [fix enforce2d](#) which corresponds to the *enforce2d* style) or as complicated as applying SHAKE constraints on bonds and angles (see [fix shake](#) which corresponds to the *shake* style) which involves many extra computations.

Here is a brief description of the class methods in `fix.h`:

|                   |   |
|-------------------|---|
| setmask           | determines when the fix is called during the timestep |
| init              | initialization before a run                           |
| setup             | called immediately before the 1st timestep            |
| initial_integrate | called at very beginning of each timestep             |
| pre_exchange      | called before atom exchange on re-neighboring steps   |
| pre_neighbor      | called before neighbor list build                     |
| post_force        | called after pair & molecular forces are computed     |
| final_integrate   | called at end of each timestep                        |

|                         |   |
|-------------------------|---|
| end_of_step             | called at very end of timestep                          |
| write_restart           | dumps fix info to restart file                          |
| restart                 | uses info from restart file to re-initialize the fix    |
| grow_arrays             | allocate memory for atom-based arrays used by fix       |
| copy_arrays             | copy atom info when an atom migrates to a new processor |
| memory_usage            | report memory used by fix                               |
| pack_exchange           | store atom's data in a buffer                           |
| unpack_exchange         | retrieve atom's data from a buffer                      |
| pack_restart            | store atom's data for writing to restart file           |
| unpack_restart          | retrieve atom's data from a restart file buffer         |
| size_restart            | size of atom's data                                     |
| maxsize_restart         | max size of atom's data                                 |
| initial_integrate_respa | same as initial_integrate, but for rRESPA               |
| post_force_respa        | same as post_force, but for rRESPA                      |
| final_integrate_respa   | same as final_integrate, but for rRESPA                 |
| pack_comm               | pack a buffer to communicate a per-atom quantity        |
| unpack_comm             |   |

|                     |  |
|---------------------|--|
|                     | unpack a buffer to communicate a per-atom quantity         |
| pack_reverse_comm   | pack a buffer to reverse communicate a per-atom quantity   |
| unpack_reverse_comm | unpack a buffer to reverse communicate a per-atom quantity |
| thermo_fields       | define quantities for thermodynamic output                 |
| thermo_compute      | compute thermodynamic quantities                           |

Typically, only a small fraction of these methods are defined for a particular fix. Setmask is mandatory, as it determines when the fix will be invoked during the timestep. Fixes that perform time integration (*nve*, *nvt*, *npt*) implement `initial_integrate` and `final_integrate` to perform velocity Verlet updates. Fixes that constrain forces implement `post_force`. Fixes that perform diagnostics typically implement `end_of_step`. For an `end_of_step` fix, one of your fix arguments must be the variable "never" which is used to determine when to call the fix. By convention, this is the first argument the fix defines (after the ID, group-ID, style).

If the fix needs to store information for each atom that persists from timestep to timestep, it can manage that memory and migrate it with the atoms as they move from processors to processor by implementing the `grow_arrays`, `copy_arrays`, `pack_exchange`, and `unpack_exchange` methods. Similarly, the `pack_restart` and `unpack_restart` methods can be implemented to store information about the fix in restart files. If you wish a integrator or force constraint fix to work with rRESPA (see the `run_style` command), the `initial_integrate`, `post_force_integrate`, and `final_integrate_respa` methods can be implemented. The `thermo_fields` and `thermo_compute` methods enable a fix to contribute values to thermodynamic output, as printed quantities and/or to be summed to the potential energy of the system.

## Atom options

All classes that define an atom style are sub-classes of the Atom class. See the `atom.h` file for a list of methods these classes defines. The atom style determines what quantities are associated with an atom in a LAMMPS simulation. If one of the existing atom styles does not define all the arrays you need to store with an atom, then a new atom class can be created.

`Atom_atomic.cpp` and `atom_atomic.h` are the simplest example of an Atom class. They implement the *atomic* style of the `atom_style` command.

Here is a brief description of the class methods in `atom.h`:



|                 |   |
|-----------------|---|
| copy            | copy info for one atom to another atom's array location             |
| pack_comm       | store an atom's info in a buffer communicated every timestep        |
| unpack_comm     | retrieve an atom's info from the buffer                             |
| pack_reverse    | store an atom's info in a buffer communicating partial forces       |
| unpack_reverse  | retrieve an atom's info from the buffer                             |
| pack_border     | store an atom's info in a buffer communicated on neighbor re-builds |
| unpack_border   | retrieve an atom's info from the buffer                             |
| pack_exchange   | store all an atom's info to migrate to another processor            |
| unpack_exchange | retrieve an atom's info from the buffer                             |

There are also several methods in atom.cpp you will need to augment with information about your new atom class, following the patterns of the other atom styles. These routines are so similar for all classes, that it was simpler to just have one master routine for all classes.

|             |   |
|-------------|---|
| constructor | create style variable and atom array ptrs to NULL |
| destructor  | free memory for atom arrays                       |
| set_style   | set style variable                                |

|                |   |
|----------------|---|
| check_style    | check for pure style vs hybrid style                      |
| style2arg      | convert style variables to keywords                       |
| grow           | re-allocate atom arrays to longer lengths                 |
| unpack_data    | parse atom lines from data file                           |
| create_one     | create an individual atom of this style                   |
| size_restart   | number of restart quantities associated with proc's atoms |
| pack_restart   | pack atom quantities into a buffer                        |
| unpack_restart | unpack atom quantities from a buffer                      |
| memory_usage   | memory allocated by atom arrays                           |

---

## Variable options

The variable class stores and evaluates input script variables \$a, \$b, ... \$z, as described in [this section](#).

*Equal*-style variables are defined by an equation that is evaluated each time the variable is used. The equation can include functions, vectors, keywords, and numbers as described in the [variable](#) command. The list of valid functions, vectors, and keywords, can be extended by adding a few lines of code to the evaluate() method at the end of the variable.cpp file. Search for the word "customize" to find the correct locations for adding code.

A new function (e.g. `foo(arg1,arg2,...)`) can be added in the section that starts with the comment

```
// customize by adding function to this list and to if statement
```

A new vector (e.g. `q`) can be added in the section that starts with the comment

```
// customize by adding vector to this list and to if statement
```

A new keyword (e.g. `mysum`) can be added in the section that starts with the comment

```
// customize by adding keyword to this list and to if statement
```

Note that keywords supported by the thermo\_style custom command are evaluated by the thermo routines, so do not need to be added to `variable.cpp`.

---

## New top-level commands

It is possible to add a new command to a LAMMPS input script as opposed to adding a new style to an existing command (`atom_style`, `pair_style`, `fix`, etc). For example the `create_atoms`, `read_data`, `velocity`, and `run` commands are all top-level LAMMPS commands that are listed in the Command section of `style.h`. When such a command is encountered in the LAMMPS input script, the topmost level of LAMMPS (`lammps.cpp`) simply creates a class with the corresponding name, invokes the "command" method of the class, and passes it the arguments from the input script. The command method can perform whatever operations it wishes on the LAMMPS data structures.

Thus to add a new command, you simply need to add a `*.cpp` and `*.h` file containing a single class:

|         |  |
|---------|--|
| command | operations<br>performed<br>by the new<br>command |
|---------|--|

Of course, the new class can define other methods and variables that it uses internally.

---

(Foo) Foo, Morefoo, and Maxfoo, J of Classic Potentials, 75, 345 (1997).

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## 9. Errors

This section describes the various kinds of errors you can encounter when using LAMMPS.

9.1 [Common problems](#)

9.2 [Reporting bugs](#)

9.3 [Error & warning messages](#)

---

## 9.1 Common problems

If two LAMMPS runs do not produce the same answer on different machines or different numbers of processors, this is typically not a bug. In theory you should get identical answers on any number of processors and on any machine. In practice, numerical round-off can cause slight differences and eventual divergence of molecular dynamics phase space trajectories within a few 100s or few 1000s of timesteps. However, the statistical properties of the two runs (e.g. average energy or temperature) should still be the same.

If the velocity command is used to set initial atom velocities, a particular atom can be assigned a different velocity when the problem on different machines. Obviously, this means the phase space trajectories of the two simulations will rapidly diverge. See the discussion of the *loop* option in the velocity command for details.

A LAMMPS simulation typically has two stages, setup and run. Most LAMMPS errors are detected at setup time; others like a bond stretching too far may not occur until the middle of a run.

LAMMPS tries to flag errors and print informative error messages so you can fix the problem. Of course LAMMPS cannot figure out your physics mistakes, like choosing too big a timestep, specifying invalid force field coefficients, or putting 2 atoms on top of each other! If you find errors that LAMMPS doesn't catch that you think it should flag, please send us an email.

If you get an error message about an invalid command in your input script, you can determine what command is causing the problem by looking in the log.lammps file or using the echo command to see it on the screen. For a given command, LAMMPS expects certain arguments in a specified order. If you mess this up, LAMMPS will often flag the error, but it may read a bogus argument and assign a value that is valid, but not what you wanted. E.g. trying to read the string "abc" as an integer value and assigning the associated variable a value of 0.

Generally, LAMMPS will print a message to the screen and exit gracefully when it encounters a fatal error. Sometimes it will print a WARNING and continue on; you can decide if the WARNING is important or not. If LAMMPS crashes or hangs without spitting out an error message first then it could be a bug (see this section) or one of the following cases:

LAMMPS runs in the available memory a processor allows to be allocated. Most reasonable MD runs are compute limited, not memory limited, so this shouldn't be a bottleneck on most platforms. Almost all large memory allocations in the code are done via C-style malloc's which will generate an error message if you run out of memory. Smaller chunks of memory are allocated via C++ "new" statements. If you are unlucky you could run out of memory just when one of these small requests is made, in which case the code will crash or hang (in parallel), since LAMMPS doesn't trap on those errors.

Illegal arithmetic can cause LAMMPS to run slow or crash. This is typically due to invalid physics and numerics that your simulation is computing. If you see wild thermodynamic values or NaN values in your LAMMPS output, something is wrong with your simulation.

In parallel, one way LAMMPS can hang is due to how different MPI implementations handle buffering of messages. If the code hangs without an error message, it may be that you need to specify an MPI setting or two (usually via an environment variable) to enable buffering or boost the sizes of messages that can be buffered.

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## 9.2 Reporting bugs

If you are confident that you have found a bug in LAMMPS, we'd like to know about it via [email](#).

First, check the "New features and bug fixes" section of the [LAMMPS WWW site](#) to see if the bug has already been reported or fixed.

If not, the most useful thing you can do for us is to isolate the problem. Run it on the smallest number of atoms and fewest number of processors and with the simplest input script that reproduces the bug.

Send an email that describes the problem and any ideas you have as to what is causing it or where in the code the problem might be. We'll request your input script and data files if necessary.

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## 9.3 Error &warning Messages

These are two alphabetic lists of the [ERROR](#) and [WARNING](#) messages LAMMPS prints out and the reason why. If the explanation here is not sufficient, the documentation for the offending command may help. Grepping the source files for the text of the error message and staring at the source code and comments is also not a bad idea! Note that sometimes the same message can be printed from multiple places in the code.

### Errors:

#### *1–3 bond count is inconsistent*

An inconsistency was detected when computing the number of 1–3 neighbors for each atom. This likely means something is wrong with the bond topologies you have defined.

#### *1–4 bond count is inconsistent*

An inconsistency was detected when computing the number of 1–4 neighbors for each atom. This likely means something is wrong with the bond topologies you have defined.

#### *All angle coeffs are not set*

All angle coefficients must be set in the data file or by the `angle_coeff` command before running a simulation.

#### *All bond coeffs are not set*

All bond coefficients must be set in the data file or by the `bond_coeff` command before running a simulation.

#### *All EAM pair coeffs are not set*

All EAM pair coefficients must be set in the data file or by the `pair_coeff` command before running a simulation.

#### *All dihedral coeffs are not set*

All dihedral coefficients must be set in the data file or by the `dihedral_coeff` command before running a simulation.

#### *All dipole moments are not set*

For atom styles that define dipole moments for each atom type, all moments must be set in the data file or by the `dipole` command before running a simulation.

#### *All improper coeffs are not set*

All improper coefficients must be set in the data file or by the `improper_coeff` command before running a simulation.

#### *All masses are not set*

For atom styles that define masses for each atom type, all masses must be set in the data file or by the `mass` command before running a simulation. They must also be set before using the `velocity` command.

#### *All pair coeffs are not set*

All pair coefficients must be set in the data file or by the `pair_coeff` command before running a simulation.

*All universe variables must have same # of values*  
Self-explanatory.

*All variables in next command must be same style*  
Self-explanatory.

*Angle atoms %d %d %d missing on proc %d at step %d*  
One or more of 3 atoms needed to compute a particular angle are missing on this processor. Typically this is because the pairwise cutoff is set too short or the angle has blown apart and an atom is too far away.

*Angle atom missing in delete\_bonds*  
The `delete_bonds` command cannot find one or more atoms in a particular angle on a particular processor. The pairwise cutoff is too short or the atoms are too far apart to make a valid angle.

*Angle atom missing in set command*  
The `set` command cannot find one or more atoms in a particular angle on a particular processor. The pairwise cutoff is too short or the atoms are too far apart to make a valid angle.

*Angle coeffs are not set*  
No angle coefficients have been assigned in the data file or via the `angle_coeff` command.

*Angle\_coeff command before angle\_style is defined*  
Coefficients cannot be set in the data file or via the `angle_coeff` command until an `angle_style` has been assigned.

*Angle\_coeff command before simulation box is defined*  
The `angle_coeff` command cannot be used before a `read_data`, `read_restart`, or `create_box` command.

*Angle\_coeff command when no angles allowed*  
The chosen atom style does not allow for angles to be defined.

*Angle coeff for hybrid has invalid style*  
Angle style hybrid uses another angle style as one of its coefficients. The angle style used in the `angle_coeff` command or read from a restart file is not recognized.

*Angles assigned incorrectly*  
Angles read in from the data file were not assigned correctly to atoms. This means there is something invalid about the topology definitions.

*Angles defined but no angle types*  
The data file header lists angles but no angle types.

*Angle style hybrid cannot have hybrid as an argument*  
Self-explanatory.

*Angle style hybrid cannot use same angle style twice*  
Self-explanatory.

*Atom count is inconsistent, cannot write restart file*  
Sum of atoms across processors does not equal initial total count. This is probably because you have lost some atoms.

*Atom IDs must be consecutive for dump dcd*  
Self-explanatory.

*Atom IDs must be consecutive for dump xtc*  
Self-explanatory.

*Atom IDs must be consecutive for dump xyz*  
Self-explanatory.

*Atom in too many rigid bodies – boost MAXBODY*  
Fix poems has a parameter `MAXBODY` (in `fix_poems.cpp`) which determines the maximum number of rigid bodies a single atom can belong to (i.e. a multibody joint). The bodies you have defined exceed this limit.

*Atom\_modify command after simulation box is defined*

The atom\_modify command cannot be used after a read\_data, read\_restart, or create\_box command.

*Atom\_modify command before atom\_style command*  
 The atom\_modify command cannot be used before an atom style has been defined.

*Atom style granular and dpd cannot be used together*  
 Self-explanatory.

*Atom style granular must perform 3d simulations*  
 Atom style granular cannot be used with 2d simulations, because the pairwise potentials are inherently 3d.

*Atom style hybrid cannot have hybrid as an argument*  
 Self-explanatory. Check the input script.

*Atom\_style command after simulation box is defined*  
 The atom\_style command cannot be used after a read\_data, read\_restart, or create\_box command.

*Attempting to rescale a 0.0 temperature*  
 Cannot rescale a temperature that is already 0.0.

*Bad FENE bond*  
 Two atoms in a FENE bond have become so far apart that the bond cannot be computed.

*Bad grid of processors*  
 The 3d grid of processors defined by the processors command does not match the number of processors LAMMPS is being run on.

*Bad principal moments*  
 Fix rigid did not compute the principal moments of inertia of a rigid group of atoms correctly.

*Bad slab parameter*  
 Kspace\_modify value for the slab/volume keyword must be  $\geq 2.0$ .

*Bitmapped lookup tables require int/float be same size*  
 Cannot use pair tables on this machine, because of word sizes. Use the pair\_modify command with table 0 instead.

*Bitmapped table is incorrect length in table file*  
 Number of table entries is not a correct power of 2.

*Bitmapped table in file does not match requested table*  
 Setting for bitmapped table in pair\_coeff command must match table in file exactly.

*Bond and angle potentials must be defined for TIP4P*  
 Cannot use TIP4P pair potential unless bond and angle potentials are defined.

*Bond atom missing in delete\_bonds*  
 The delete\_bonds command cannot find one or more atoms in a particular bond on a particular processor. The pairwise cutoff is too short or the atoms are too far apart to make a valid bond.

*Bond atom missing in set command*  
 The set command cannot find one or more atoms in a particular bond on a particular processor. The pairwise cutoff is too short or the atoms are too far apart to make a valid bond.

*Bond atoms %d %d missing on proc %d at step %d*  
 One or more of 2 atoms needed to compute a particular bond are missing on this processor. Typically this is because the pairwise cutoff is set too short or the bond has blown apart and an atom is too far away.

*Bond coeff for hybrid has invalid style*  
 Bond style hybrid uses another bond style as one of its coefficients. The bond style used in the bond\_coeff command or read from a restart file is not recognized.

*Bond\_coeff command before bond\_style is defined*  
 Coefficients cannot be set in the data file or via the bond\_coeff command until an bond\_style has been assigned.

*Bond\_coeff command before simulation box is defined*  
 The bond\_coeff command cannot be used before a read\_data, read\_restart, or create\_box command.

*Bond\_coeff command when no bonds allowed*

The chosen atom style does not allow for bonds to be defined.

*Bond coeffs are not set*  
No bond coefficients have been assigned in the data file or via the `bond_coeff` command.

*Bond potential must be defined for SHAKE*  
Cannot use fix shake unless bond potential is defined.

*Bonds assigned incorrectly*  
Bonds read in from the data file were not assigned correctly to atoms. This means there is something invalid about the topology definitions.

*Bonds defined but no bond types*  
The data file header lists bonds but no bond types.

*Bond style hybrid cannot have hybrid as an argument*  
Self-explanatory. Check the input script.

*Bond style hybrid cannot use same bond style twice*  
The sub-style arguments of `bond_style hybrid` cannot be duplicated. Check the input script.

*Bond style quartic cannot be used with 3,4-body interactions*  
No angle, dihedral, or improper styles can be defined when using bond style quartic.

*Both sides of boundary must be periodic*  
Cannot specify a boundary as periodic only on the lo or hi side. Must be periodic on both sides.

*Boundary command after simulation box is defined*  
The boundary command cannot be used after a `read_data`, `read_restart`, or `create_box` command.

*Box bounds are invalid*  
The box boundaries specified in the `read_data` file are invalid. The lo value must be less than the hi value for all 3 dimensions.

*Can only wiggle zcylinder wall in z dim*  
The Self-explanatory.

*Cannot change dump\_modify every for dump dcd*  
The frequency of writing dump dcd snapshots cannot be changed.

*Cannot compute PPPM G*  
LAMMPS failed to compute a valid approximation for the PPPM `g_ewald` factor that partitions the computation between real space and k-space.

*Cannot compute PPPM X grid spacing*  
LAMMPS failed to compute a valid PPPM grid spacing in the x dimension.

*Cannot compute PPPM Y grid spacing*  
LAMMPS failed to compute a valid PPPM grid spacing in the y dimension.

*Cannot compute PPPM Z grid spacing*  
LAMMPS failed to compute a valid PPPM grid spacing in the z dimension.

*Cannot create atoms with undefined lattice*  
Must use the lattice command before using the `create_atoms` command.

*Cannot create\_box after simulation box is defined*  
The `create_box` command cannot be used after a `read_data`, `read_restart`, or `create_box` command.

*Cannot create\_box until atom\_style is defined*  
Self-explanatory.

*Cannot create vels with loop all for non-contiguous atom IDs*  
You cannot use the loop all option if you atom IDs do not span 1 to natoms

*Cannot evaluate variable equal command*  
Syntax or keyword names in mathematical expression are not recognized.

*Cannot find delete\_bonds group ID*  
Group ID used in the `delete_bonds` command does not exist.

*Cannot find set command group ID*  
Group ID used in the `set` command does not exist.

*Cannot fix nph on a non-periodic dimension*



Pressure can only be controlled on a dimension that is periodic.

*Cannot fix npt on a non-periodic dimension*  
 Pressure can only be controlled on a dimension that is periodic.

*Cannot fix volume/rescale on a non-periodic boundary*  
 Volume can only be rescaled on a dimension that is periodic.

*Cannot fix uniaxial on non-periodic system*  
 Volume can only be rescaled uniaxially if system is periodic in all 3 dimensions.

*Cannot invoke single() with pairwise TIP4P potential*  
 Commands that invoke the single() function within pairwise potentials cannot be used with a TIP4P potential, due to the way it computes forces on other atoms besides the i,j pair. This includes the eng and stress tensor components for the dump custom command.

*Cannot open EAM potential file %s*  
 The specified EAM potential file cannot be opened. Check that the path and name are correct.

*Cannot open file %s*  
 The specified file cannot be opened. Check that the path and name are correct.

*Cannot open fix com file %s*  
 The output file for the fix com command cannot be opened. Check that the path and name are correct.

*Cannot open fix gran/diag file %s*  
 The output file for the fix gran/diag command cannot be opened. Check that the path and name are correct.

*Cannot open fix msd file %s*  
 The output file for the fix msd command cannot be opened. Check that the path and name are correct.

*Cannot open fix poems file %s*  
 The specified file cannot be opened. Check that the path and name are correct.

*Cannot open fix rdf file %s*  
 The output file for the fix rdf command cannot be opened. Check that the path and name are correct.

*Cannot open fix tmd file %s*  
 The output file for the fix tmd command cannot be opened. Check that the path and name are correct.

*Cannot open gzipped file*  
 LAMMPS is attempting to open a gzipped version of the specified file but was unsuccessful. Check that the path and name are correct.

*Cannot open pair\_write file*  
 The specified output file for pair energies and forces cannot be opened. Check that the path and name are correct.

*Cannot open restart file %s*  
 The output restart file cannot be opened. Check that the path and name are correct and that disk space is available.

*Cannot read\_data after simulation box is defined*  
 The read\_data command cannot be used after a read\_data, read\_restart, or create\_box command.

*Cannot read\_data until atom\_style is defined*  
 Self-explanatory.

*Cannot read\_restart after simulation box is defined*  
 The read\_restart command cannot be used after a read\_data, read\_restart, or create\_box command.

*Cannot redefine variable as a different style*  
 The variable was already used as a different style variable.

*Cannot replicate 2d simulation in z dimension*  
 The replicate command cannot replicate a 2d simulation in the z dimension.

*Cannot replicate with fixes that store atom quantities*  
 Either fixes are defined that create and store atom-based vectors or a restart file was read which included atom-based vectors for fixes. The replicate command cannot duplicate that information for new atoms. You should use the replicate command before fixes are applied to the system.

*Cannot run 2d simulation with nonperiodic Z dimension*

Use the boundary command to make the z dimension periodic in order to run a 2d simulation.

*Cannot set both respa pair and inner/middle/outer*

In the rRESPA integrator, you must compute pairwise potentials either all together (pair), or in pieces (inner/middle/outer). You can't do both.

*Cannot set dipole for this atom style*

This atom style does not support dipole settings for each atom type.

*Cannot set dump\_modify flush for dump xtc*

Self-explanatory.

*Cannot set mass for this atom style*

This atom style does not support mass settings for each atom type. Instead they are defined on a per-atom basis in the data file.

*Cannot set respa middle without inner/outer*

In the rRESPA integrator, you must define both a inner and outer setting in order to use a middle setting.

*Cannot set these values with this atom style*

Choice of set style does not match attribute of atom style.

*Cannot use atom style granular with chosen thermo settings*

Cannot output temperature or pressure with atom style granular.

*Cannot use delete\_bonds with non-molecular system*

Your choice of atom style does not have bonds.

*Cannot use dump bond with non-molecular system*

Your choice of atom style does not have bonds.

*Cannot use Ewald with 2d simulation*

The kspace style ewald cannot be used in 2d simulations. You can use 2d Ewald in a 3d simulation; see the kspace\_modify command.

*Cannot use fix gravity vector with atom style granular*

Self-explanatory.

*Cannot use fix poems with atom style granular*

This fix is not yet enabled for this atom style.

*Cannot use fix rigid with atom style granular*

This fix is not yet enabled for this atom style.

*Cannot use fix shake with non-molecular system*

Your choice of atom style does not have bonds.

*Cannot use multiple long-range potentials with pair hybrid*

Only one sub-style potential with a long-range component can be used with pair\_style hybrid.

*Cannot use nonperiodic boundaries with Ewald*

For kspace style ewald, all 3 dimensions must have periodic boundaries unless you use the kspace\_modify command to define a 2d slab with a non-periodic z dimension.

*Cannot use nonperiodic boundaries with PPPM*

For kspace style pppm, All 3 dimensions must have periodic boundaries unless you use the kspace\_modify command to define a 2d slab with a non-periodic z dimension.

*Cannot use PPPM with 2d simulation*

The kspace style pppm cannot be used in 2d simulations. You can use 2d PPPM in a 3d simulation; see the kspace\_modify command.

*Cannot use region INF when box does not exist*

Regions that extend to the box boundaries can only be used after the create\_box command has been used.

*Cannot use vectors in variables unless atom map exists*

Vectors require an atom map to be able to lookup the vector index. Only atom styles with molecular information creat a global map.

*Cannot zero momentum for less than 2 atoms*

Velocity command is being used with momentum-zeroing options on a group with 0 or 1 atoms.

*Command-line variable already exists*

Cannot use the `-var` command-line option to define the same variable more than once.

*Could not create 3d FFT plan*

The FFT setup in pppm failed.

*Could not create 3d remap plan*

The FFT setup in pppm failed.

*Could not find delete\_atoms group ID*

Group ID used in the `delete_atoms` command does not exist.

*Could not find delete\_atoms region ID*

Region ID used in the `delete_atoms` command does not exist.

*Could not find displace\_atoms group ID*

A group ID used in the `displace_atoms` command does not exist.

*Could not find dump\_modify ID*

A dump ID used in the `dump_modify` command does not exist.

*Could not find dump group ID*

A group ID used in the `dump` command does not exist.

*Could not find fix group ID*

A group ID used in the `fix` command does not exist.

*Could not find fix poeoms group ID*

A group ID used in the `fix poeoms` command does not exist.

*Could not find fix rigid group ID*

A group ID used in the `fix rigid` command does not exist.

*Could not find fix\_modify ID*

A fix ID used in the `fix_modify` command does not exist.

*Could not find fix\_modify temperature ID*

A temperature ID used in the `fix_modify` command does not exist.

*Could not find fix spring vector group ID*

Group ID used with `fix spring` command does not exist.

*Could not find temp\_modify ID*

A temperature ID used in the `temp_modify` command does not exist.

*Could not find temperature group ID*

A group ID used in the `temperature` command does not exist.

*Could not find thermo temperature ID*

A temperature ID used in the `thermo` custom style does not exist.

*Could not find thermo\_modify temperature ID*

A temperature ID used in the `thermo_modify` command does not exist.

*Could not find undump ID*

A dump ID used in the `undump` command does not exist.

*Could not find unfix ID*

A fix ID used in the `unfix` command does not exist.

*Could not find velocity group ID*

A group ID used in the `velocity` command does not exist.

*Could not find velocity temperature ID*

A temperature ID used in the `velocity` command does not exist.

*Could not open dump file*

The output file for the `dump` command cannot be opened. Check that the path and name are correct.

*Could not open input script*

The input script file named in a command-line argument could not be opened.

*Could not open log.lammps*

The default LAMMPS log file cannot be opened. Check that the directory you are running in allows for files to be created.

*Could not open logfile*

The LAMMPS log file named in a command-line argument cannot be opened. Check that the path and name are correct.

*Could not open logfile %s*

The LAMMPS log file specified in the input script cannot be opened. Check that the path and name are correct.

*Could not open new input file %s*

The input script file named in an include or jump command could not be opened. Check that the path and name are correct.

*Could not open screen file*

The screen file specified as a command-line argument cannot be opened. Check that the directory you are running in allows for files to be created.

*Could not open universe log file*

For a multi-partition run, the master log file cannot be opened. Check that the directory you are running in allows for files to be created.

*Could not open universe screen file*

For a multi-partition run, the master screen file cannot be opened. Check that the directory you are running in allows for files to be created.

*Create\_atoms command before simulation box is defined*

The create\_atoms command cannot be used before a read\_data, read\_restart, or create\_box command.

*Create\_atoms region ID does not exist*

A region ID used in the create\_atoms command does not exist.

*Create\_box region must be of type inside*

The region used in the create\_box command must not be an "outside" region. See the region command for details.

*Create\_box region ID does not exist*

A region ID used in the create\_box command does not exist.

*Cyclic loop in joint connections*

Fix poems cannot (yet) work with coupled bodies whose joints connect the bodies in a ring (or cycle).

*Delete\_atoms command before simulation box is defined*

The delete\_atoms command cannot be used before a read\_data, read\_restart, or create\_box command.

*Delete\_atoms cutoff > neighbor cutoff*

Cannot use a cutoff with delete\_atoms overlap that is larger than the force cutoff + neighbor skin.

*Delete\_bonds command before simulation box is defined*

The delete\_bonds command cannot be used before a read\_data, read\_restart, or create\_box command.

*Delete\_bonds command with no atoms existing*

No atoms are yet defined so the delete\_bonds command cannot be used.

*Did not assign all atoms correctly*

Atoms read in from a data file were not assigned correctly to processors. This is likely due to some atom coordinates being outside a non-periodic simulation box.

*Did not find keyword in table file*

Keyword used in pair\_coeff command was not found in table file.

*Did not find fix shake partner info*

Could not find bond partners implied by fix shake command. This error can be triggered if the delete\_bonds command was used before fix shake, and it removed bonds without resetting the 1-2, 1-3, 1-4 weighting list via the special keyword.

*Dihedral atoms %d %d %d %d missing on proc %d at step %d*

One or more of 4 atoms needed to compute a particular dihedral are missing on this processor.

Typically this is because the pairwise cutoff is set too short or the dihedral has blown apart and an

atom is too far away.

*Dihedral atom missing in delete\_bonds*  
The delete\_bonds command cannot find one or more atoms in a particular dihedral on a particular processor. The pairwise cutoff is too short or the atoms are too far apart to make a valid dihedral.

*Dihedral atom missing in set command*  
The set command cannot find one or more atoms in a particular dihedral on a particular processor. The pairwise cutoff is too short or the atoms are too far apart to make a valid dihedral.

*Dihedral\_coeff command before dihedral\_style is defined*  
Coefficients cannot be set in the data file or via the dihedral\_coeff command until an dihedral\_style has been assigned.

*Dihedral\_coeff command before simulation box is defined*  
The dihedral\_coeff command cannot be used before a read\_data, read\_restart, or create\_box command.

*Dihedral\_coeff command when no dihedrals allowed*  
The chosen atom style does not allow for dihedrals to be defined.

*Dihedral\_coeff for hybrid has invalid style*  
Dihedral style hybrid uses another dihedral style as one of its coefficients. The dihedral style used in the dihedral\_coeff command or read from a restart file is not recognized.

*Dihedral coeffs are not set*  
No dihedral coefficients have been assigned in the data file or via the dihedral\_coeff command.

*Dihedrals assigned incorrectly*  
Dihedrals read in from the data file were not assigned correctly to atoms. This means there is something invalid about the topology definitions.

*Dihedrals defined but no dihedral types*  
The data file header lists dihedrals but no dihedral types.

*Dihedral style hybrid cannot have hybrid as an argument*  
Self-explanatory.

*Dihedral style hybrid cannot use same dihedral style twice*  
Self-explanatory.

*Dimension command after simulation box is defined*  
The dimension command cannot be used after a read\_data, read\_restart, or create\_box command.

*Dipole command before simulation box is defined*  
The dipole command cannot be used before a read\_data, read\_restart, or create\_box command.

*Displace\_atoms command before simulation box is defined*  
The displace\_atoms command cannot be used before a read\_data, read\_restart, or create\_box command.

*Dump dcd must use group all*  
Self-explanatory.

*Dump dcd of non-matching # of atoms*  
Every snapshot written by dump dcd must contain the same # of atoms.

*Dump xtc must use group all*  
Self-explanatory.

*Dump\_modify region ID does not exist*  
Self-explanatory.

*Dump xtc must use group all*  
Self-explanatory.

*Failed to allocate %d bytes for array %s*  
Your LAMMPS simulation has run out of memory. You need to run a smaller simulation or on more processors.

*Failed to reallocate %d bytes for array %s*

Your LAMMPS simulation has run out of memory. You need to run a smaller simulation or on more processors.

*Fix command before simulation box is defined*  
The fix command cannot be used before a read\_data, read\_restart, or create\_box command.

*Fix insert region ID does not exist*  
A region ID used in the fix insert command does not exist.

*Fix langevin period must be > 0.0*  
The time window for temperature relaxation must be > 0

*Fix langevin region ID does not exist*  
Self-explanatory.

*Fix nph periods must be > 0.0*  
The time window for pressure relaxation must be > 0

*Fix npt periods must be > 0.0*  
The time window for temperature or pressure relaxation must be > 0

*Fix nvt period must be > 0.0*  
The time window for temperature relaxation must be > 0

*Fix orient/fcc file open failed*  
The fix orient/fcc command could not open a specified file.

*Fix orient/fcc file read failed*  
The fix orient/fcc command could not read the needed parameters from a specified file.

*Fix orient/fcc found self twice*  
The neighbor lists used by fix orient/fcc are messed up. If this error occurs, it is likely a bug, so send an email.

*Fix rdf requires a pair style be defined*  
Cannot use the rdf fix unless a pair style with a cutoff has been defined.

*Fix temp/rescale region ID does not exist*  
Self-explanatory.

*Fix tmd must come after integration fixes*  
Any fix tmd command must appear in the input script after all time integration fixes (nve, nvt, npt).  
See the fix tmd documentation for details.

*Fix wall/gran can only be used with granular pair style*  
Self-explanatory.

*Granular pair styles do not use pair\_coeff settings*  
The pair\_coeff command cannot be used with granular force fields.

*Gravity must point in -z to use with fix insert*  
The fix insert command assumes the theta angle for gravity is 180.0.

*Group command before simulation box is defined*  
The group command cannot be used before a read\_data, read\_restart, or create\_box command.

*Group ID does not exist*  
A group ID used in the group command does not exist.

*Group region ID does not exist*  
A region ID used in the group command does not exist.

*Illegal ... command*  
Self-explanatory. Check the input script syntax and compare to the documentation for the command.

*Improper atoms %d %d %d %d missing on proc %d at step %d*  
One or more of 4 atoms needed to compute a particular improper are missing on this processor.  
Typically this is because the pairwise cutoff is set too short or the improper has blown apart and an atom is too far away.

*Improper atom missing in delete\_bonds*  
The delete\_bonds command cannot find one or more atoms in a particular improper on a particular processor. The pairwise cutoff is too short or the atoms are too far apart to make a valid improper.

*Improper atom missing in set command*

The set command cannot find one or more atoms in a particular improper on a particular processor.  
The pairwise cutoff is too short or the atoms are too far apart to make a valid improper.

*Improper\_coeff command before improper\_style is defined*

Coefficients cannot be set in the data file or via the improper\_coeff command until an improper\_style has been assigned.

*Improper\_coeff command before simulation box is defined*

The improper\_coeff command cannot be used before a read\_data, read\_restart, or create\_box command.

*Improper\_coeff command when no impropers allowed*

The chosen atom style does not allow for impropers to be defined.

*Improper coeff for hybrid has invalid style*

Improper style hybrid uses another improper style as one of its coefficients. The improper style used in the improper\_coeff command or read from a restart file is not recognized.

*Improper coeffs are not set*

No improper coefficients have been assigned in the data file or via the improper\_coeff command.

*Impropers assigned incorrectly*

Impropers read in from the data file were not assigned correctly to atoms. This means there is something invalid about the topology definitions.

*Impropers defined but no improper types*

The data file header lists improper but no improper types.

*Improper style hybrid cannot have hybrid as an argument*

Self-explanatory.

*Improper style hybrid cannot use same improper style twice*

Self-explanatory.

*Inconsistent dipole settings for some atoms*

Dipole moment must be 0 for non-dipole type atoms. Dipole moment must be set for dipole type atoms.

*Incorrect args for angle coefficients*

Self-explanatory. Check the input script or data file.

*Incorrect args for bond coefficients*

Self-explanatory. Check the input script or data file.

*Incorrect args for dihedral coefficients*

Self-explanatory. Check the input script or data file.

*Incorrect args for improper coefficients*

Self-explanatory. Check the input script or data file.

*Incorrect args for pair coefficients*

Self-explanatory. Check the input script or data file.

*Incorrect atom format in data file*

Number of values per atom line in the data file is not consistent with the atom style.

*Incorrect boundaries with slab Ewald*

Must have periodic x,y dimensions and non-periodic z dimension to use 2d slab option with Ewald.

*Incorrect boundaries with slab PPPM*

Must have periodic x,y dimensions and non-periodic z dimension to use 2d slab option with PPPM.

*Incorrect format in TMD target file*

Format of file read by fix tmd command is incorrect.

*Incorrect multiplicity arg for dihedral coefficients*

Self-explanatory. Check the input script or data file.

*Incorrect sign arg for dihedral coefficients*

Self-explanatory. Check the input script or data file.

*Incorrect weight arg for dihedral coefficients*

Self-explanatory. Check the input script or data file.

*Insertion region extends outside simulation box*  
 Region specified with fix insert command extends outside the global simulation box.

*Insufficient Jacobi rotations for POEMS body*  
 Eigensolve for rigid body was not sufficiently accurate.

*Insufficient Jacobi rotations for rigid body*  
 Eigensolve for rigid body was not sufficiently accurate.

*Invalid \$ variable*  
 The character following a \$ in the input script is not between "a" and "z".

*Invalid angle style*  
 The choice of angle style is unknown.

*Invalid angle type in Angles section of data file*  
 Angle type must be positive integer and within range of specified angle types.

*Invalid angle type index for fix shake*  
 Self-explanatory.

*Invalid atom ID in Angles section of data file*  
 Atom IDs must be positive integers and within range of defined atoms.

*Invalid atom ID in Atoms section of data file*  
 Atom IDs must be positive integers.

*Invalid atom ID in Bonds section of data file*  
 Atom IDs must be positive integers and within range of defined atoms.

*Invalid atom ID in Dihedrals section of data file*  
 Atom IDs must be positive integers and within range of defined atoms.

*Invalid atom ID in Improvers section of data file*  
 Atom IDs must be positive integers and within range of defined atoms.

*Invalid atom ID in Velocities section of data file*  
 Atom IDs must be positive integers and within range of defined atoms.

*Invalid atom mass for fix shake*  
 Mass specified in fix shake command must be > 0.0.

*Invalid atom style*  
 The choice of atom style is unknown.

*Invalid atom type in Atoms section of data file*  
 Atom types must range from 1 to specified # of types.

*Invalid atom type in neighbor exclusion list*  
 Atom types must range from 1 to Ntypes inclusive.

*Invalid atom type index for fix shake*  
 Atom types must range from 1 to Ntypes inclusive.

*Invalid atom types in fix rdf command*  
 Atom types must range from 1 to Ntypes inclusive.

*Invalid atom types in pair\_write command*  
 Atom types must range from 1 to Ntypes inclusive.

*Invalid bond style*  
 The choice of bond style is unknown.

*Invalid bond type in Bonds section of data file*  
 Bond type must be positive integer and within range of specified bond types.

*Invalid bond type index for fix shake*  
 Self-explanatory. Check the fix shake command in the input script.

*Invalid coeffs for this angle style*  
 Cannot set class 2 coeffs in data file for this angle style.

*Invalid coeffs for this dihedral style*  
 Cannot set class 2 coeffs in data file for this dihedral style.



*Invalid coeffs for this improper style*

Cannot set class 2 coeffs in data file for this improper style.

*Invalid command–line argument*

One or more command–line arguments is invalid. Check the syntax of the command you are using to launch LAMMPS.

*Invalid cutoffs in pair\_write command*

Inner cutoff must be larger than 0.0 and less than outer cutoff.

*Invalid data file section: Angle Coeffs*

Atom style does not allow angles.

*Invalid data file section: AngleAngle Coeffs*

Atom style does not allow impropers.

*Invalid data file section: AngleAngleTorsion Coeffs*

Atom style does not allow dihedrals.

*Invalid data file section: AngleTorsion Coeffs*

Atom style does not allow dihedrals.

*Invalid data file section: Angles*

Atom style does not allow angles.

*Invalid data file section: Bond Coeffs*

Atom style does not allow bonds.

*Invalid data file section: BondAngle Coeffs*

Atom style does not allow angles.

*Invalid data file section: BondBond Coeffs*

Atom style does not allow angles.

*Invalid data file section: BondBond13 Coeffs*

Atom style does not allow dihedrals.

*Invalid data file section: Bonds*

Atom style does not allow bonds.

*Invalid data file section: Dihedral Coeffs*

Atom style does not allow dihedrals.

*Invalid data file section: Dihedrals*

Atom style does not allow dihedrals.

*Invalid data file section: EndBondTorsion Coeffs*

Atom style does not allow dihedrals.

*Invalid data file section: Improper Coeffs*

Atom style does not allow impropers.

*Invalid data file section: Impropers*

Atom style does not allow impropers.

*Invalid data file section: MiddleBondTorsion Coeffs*

Atom style does not allow dihedrals.

*Invalid dihedral style*

The choice of dihedral style is unknown.

*Invalid dihedral type in Dihedrals section of data file*

Dihedral type must be positive integer and within range of specified dihedral types.

*Invalid dump dcd filename*

Filenames used with the dump dcd style cannot be binary or compressed or cause multiple files to be written.

*Invalid dump frequency*

Dumps frequency must be 1 or greater.

*Invalid dump\_modify threshold operator*

Operator keyword used for threshold specification is not recognized.

*Invalid dump style*

The choice of dump style is unknown.

*Invalid dump xtc filename*  
 Filenames used with the dump xtc style cannot be binary or compressed or cause multiple files to be written.

*Invalid dump xyz filename*  
 Filenames used with the dump xyz style cannot be binary or cause files to be written by each processor.

*Invalid group ID in neigh\_modify command*  
 A group ID used in the neigh\_modify command does not exist.

*Invalid fix style*  
 The choice of fix style is unknown.

*Invalid flag in header of restart file*  
 Value read from beginning of restart file is not recognized.

*Invalid improper style*  
 The choice of improper style is unknown.

*Invalid improper type in Improvers section of data file*  
 Improper type must be positive integer and within range of specified improper types.

*Invalid keyword in dump custom command*  
 One or more attribute keywords are not recognized.

*Invalid keyword in pair table parameters*  
 Keyword used in list of table parameters is not recognized.

*Invalid keyword in thermo\_style command*  
 One or more attribute keywords are not recognized.

*Invalid keyword in variable equal command*  
 One or more attribute keywords are not recognized.

*Invalid kspace style*  
 The choice of kspace style is unknown.

*Invalid natoms for dump dcd*  
 Natoms is initially 0 which is not valid for the dump dcd style. Natoms must be constant for the duration of the simulation.

*Invalid natoms for dump xtc*  
 Natoms is initially 0 which is not valid for the dump xtc style.

*Invalid natoms for dump xyz*  
 Natoms is initially 0 which is not valid for the dump xyz style.

*Invalid order of forces within respa levels*  
 For respa, ordering of force computations within respa levels must obey certain rules. E.g. bonds cannot be compute less frequently than angles, pairwise forces cannot be computed less frequently than kspace, etc.

*Invalid pair style*  
 The choice of pair style is unknown.

*Invalid pair table cutoff*  
 Cutoffs in pair\_coeff command are not valid with read-in pair table.

*Invalid pair table length*  
 Length of read-in pair table is invalid

*Invalid random number seed in set command*  
 Random number seed must be > 0.

*Invalid region style*  
 The choice of region style is unknown.

*Invalid style in pair\_write command*  
 Self-explanatory. Check the input script.

*Invalid temperature style*

The choice of temperature style is unknown.

*Invalid type for dipole set*  
Dipole command must set a type from 1–N where N is the number of atom types.

*Invalid type for mass set*  
Mass command must set a type from 1–N where N is the number of atom types.

*Invalid type in set command*  
Type used in set command must be from 1–N where N is the number of atom types (bond types, angle types, etc).

*Invalid variable in command–line argument*  
Command–line arg –var must set a variable from "a" to "z".

*Invalid variable in next command*  
Next command in input script must set variables from "a" to "z".

*Invalid variable in variable command*  
Variable command in input script must set a variable from "a" to "z".

*Invalid variable style with next command*  
Variable styles *equal* and *world* cannot be used in a next command.

*Invalid vector in variable equal command*  
One or more vector names are not recognized.

*KSpace style has not yet been set*  
Cannot use kspace\_modify command until a kspace style is set.

*KSpace style is incompatible with Pair style*  
Setting a kspace style requires that a pair style with a long–range Coulombic component be selected.

*Label wasn't found in input script*  
Self–explanatory.

*Lattice style incompatible with dimension*  
2d simulation can use sq, sq2, or hex lattice. 3d simulation can use sc, bcc, or fcc lattice.

*Lost atoms via displacement: original %.15g current %.15g*  
Moving atoms via the displace\_atoms command lost one or more atoms.

*Lost atoms: original %.15g current %.15g*  
A thermodynamic computation has detected lost atoms.

*Marsaglia RNG cannot use 0 seed*  
The random number generator use for the fix langevin command cannot use 0 as an initial seed.

*Mass command before simulation box is defined*  
The mass command cannot be used before a read\_data, read\_restart, or create\_box command.

*Minimize command before simulation box is defined*  
The minimize command cannot be used before a read\_data, read\_restart, or create\_box command.

*Min\_style command before simulation box is defined*  
The min\_style command cannot be used before a read\_data, read\_restart, or create\_box command.

*More than one freeze fix*  
You can only define one freeze fix.

*More than one shake fix*  
You can only define one SHAKE fix.

*Must define angle\_style before Angle Coeffs*  
Must use an angle\_style command before reading a data file that defines Angle Coeffs.

*Must define angle\_style before BondAngle Coeffs*  
Must use an angle\_style command before reading a data file that defines Angle Coeffs.

*Must define angle\_style before BondBond Coeffs*  
Must use an angle\_style command before reading a data file that defines Angle Coeffs.

*Must define bond\_style before Bond Coeffs*  
Must use a bond\_style command before reading a data file that defines Bond Coeffs.

*Must define dihedral\_style before AngleAngleTorsion Coeffs*

Must use a `dihedral_style` command before reading a data file that defines AngleAngleTorsion Coeffs.  
*Must define dihedral\_style before AngleTorsion Coeffs*  
 Must use a `dihedral_style` command before reading a data file that defines AngleTorsion Coeffs.  
*Must define dihedral\_style before BondBond13 Coeffs*  
 Must use a `dihedral_style` command before reading a data file that defines BondBond13 Coeffs.  
*Must define dihedral\_style before Dihedral Coeffs*  
 Must use a `dihedral_style` command before reading a data file that defines Dihedral Coeffs.  
*Must define dihedral\_style before EndBondTorsion Coeffs*  
 Must use a `dihedral_style` command before reading a data file that defines EndBondTorsion Coeffs.  
*Must define dihedral\_style before MiddleBondTorsion Coeffs*  
 Must use a `dihedral_style` command before reading a data file that defines MiddleBondTorsion Coeffs.  
*Must define improper\_style before AngleAngle Coeffs*  
 Must use an `improper_style` command before reading a data file that defines AngleAngle Coeffs.  
*Must define improper\_style before Improper Coeffs*  
 Must use an `improper_style` command before reading a data file that defines Improper Coeffs.  
*Must define pair\_style before Pair Coeffs*  
 Must use a `pair_style` command before reading a data file that defines Pair Coeffs.  
*Must have more than one processor partition to temper*  
 Cannot use the `temper` command with only one processor partition. Use the `-partition` command-line option.  
*Must read Atoms before Angles*  
 The Atoms section of a data file must come before an Angles section.  
*Must read Atoms before Bonds*  
 The Atoms section of a data file must come before a Bonds section.  
*Must read Atoms before Dihedrals*  
 The Atoms section of a data file must come before a Dihedrals section.  
*Must read Atoms before Improvers*  
 The Atoms section of a data file must come before an Improvers section.  
*Must read Atoms before Velocities*  
 The Atoms section of a data file must come before a Velocities section.  
*Must set both respa inner and outer*  
 Cannot use just the inner or outer option with `respa` without using the other.  
*Must specify a region in fix insert*  
 Self-explanatory.  
*Must use -in switch with multiple partitions*  
 A multi-partition simulation cannot read the input script from `stdin`. The `-in` command-line option must be used to specify a file.  
*Must use a block or cylinder region with fix insert*  
 Self-explanatory.  
*Must use a molecular atom style with fix poems molecule*  
 Self-explanatory.  
*Must use a molecular atom style with fix rigid molecule*  
 Self-explanatory.  
*Must use molecular atom style with neigh\_modify exclude molecule*  
 Self-explanatory.  
*Must use a z-axis cylinder with fix insert*  
 The axis of the cylinder region used with the `fix insert` command must be oriented along the `z` dimension.  
*Must use atom style dpd with pair style dpd*  
 Self-explanatory.

*Must use atom style granular with lj units*

Self-explanatory.

*Must use atom style granular with pair style granular*

Self-explanatory.

*Must use atom style granular with chosen thermo settings*

If granular thermo info is to be output, must use atom style granular.

*Must use atom style granular with granular thermo output*

If atom style is granular, must use thermo style granular or custom.

*Must use charged atom style with fix efield*

The atom style being used does not allow atoms to have assigned charges. Hence it will not work with this fix which generates a force due to an E-field acting on charge.

*Must use charged atom style with this pair style*

The atom style being used does not allow atoms to have assigned charges. Hence it will not work with this choice of pair style.

*Must use fix freeze with atom style granular*

Self-explanatory.

*Must use fix gran/diag with atom style granular*

Self-explanatory.

*Must use fix gran/diag with granular pair style*

Self-explanatory.

*Must use fix gravity chute with atom style granular*

Self-explanatory.

*Must use fix gravity spherical with atom style granular*

Self-explanatory.

*Must use fix gravity gradient with atom style granular*

Self-explanatory.

*Must use fix gravity with fix insert*

Insertion of granular particles must be done under the influence of gravity.

*Must use fix insert with atom style granular*

Self-explanatory.

*Must use fix nve/gran with atom style granular*

Self-explanatory.

*Must use fix wall/gran with atom style granular*

Self-explanatory.

*Must use newton pairwise on with TIP4P potential*

Use of a TIP4P pair potential requires the newton command setting for pairwise interactions be "on", because of the way forces are computed on other atoms due to TIP4P interactions.

*Must use region with side = in with fix insert*

Self-explanatory.

*Must use special bonds = 1,1,1 with bond style quartic*

The settings for the special\_bonds command must be set as indicated when using bond style quartic.

*Needed topology not in data file*

The header of the data file indicated that bonds or angles or dihedrals or impropers would be included, but they were not present.

*Neighbor delay must be 0 or multiple of every setting*

The delay and every parameters set via the neigh\_modify command are inconsistent. If the delay setting is non-zero, then it must be a multiple of the every setting.

*Neighbor list overflow, boost neigh\_modify one or page*

There are too many neighbors of a single atom. Use the neigh\_modify command to increase the neighbor page size and the max number of neighbors allowed for one atom.

*Newton bond change after simulation box is defined*

The newton command cannot be used to change the newton bond value after a read\_data, read\_restart, or create\_box command.

*No angles allowed with this atom style*  
Self-explanatory. Check data file.

*No atoms in data file*  
The header of the data file indicated that atoms would be included, but they were not present.

*No atoms to compute diffusion for*  
The fix msd command has no atoms to compute on.

*No bonds allowed with this atom style*  
Self-explanatory. Check data file.

*No dihedrals allowed with this atom style*  
Self-explanatory. Check data file.

*No dump custom arguments specified*  
The dump custom command requires that atom quantities be specified to output to dump file.

*No impropers allowed with this atom style*  
Self-explanatory. Check data file.

*No rigid bodies defined by fix rigid*  
Self-explanatory.

*Non integer # of swaps in temper command*  
Swap frequency in temper command must evenly divide the total # of timesteps.

*Non-orthogonal lattice vectors*  
Self-explanatory.

*One or zero atoms in rigid body*  
Any rigid body defined by the fix rigid command must contain 2 or more atoms.

*One or more atoms belong to multiple rigid bodies*  
Two or more rigid bodies defined by the fix rigid command cannot contain the same atom.

*Orientation vectors are not right-handed*  
The 3 vectors defined by the orient command must form a right-handed coordinate system.

*Out of range atoms – cannot compute PPPM*  
One or more atoms are attempting to map their charge to a PPPM grid point that is not owned by a processor. This is usually because an atom has moved to far in a single timestep.

*Pair distance < table inner cutoff*  
Two atoms are closer together than the pairwise table allows.

*Pair distance > table outer cutoff*  
Two atoms are further apart than the pairwise table allows.

*Pair style must be defined to use bond style quartic*  
Bond style quartic requires a pair style be defined.

*Pair table parameters did not set N*  
List of pair table parameters must include N setting.

*PPPM grid is too large*  
The global PPPM grid is larger than OFFSET in one or more dimensions. OFFSET is currently set to 4096. You likely need to decrease the requested precision.

*PPPM order cannot be greater than %d*  
Self-explanatory.

*PPPM stencil extends too far, reduce PPPM order*  
The grid points that atom charge are mapped to cannot extend further than one neighbor processor away. Reducing the PPPM order via the kspace\_modify command will reduce the stencil distance.

*Pair coeff for hybrid has invalid style*  
Style in pair coeff must have been listed in pair\_style command.

*Pair cutoff < Respa interior cutoff*  
One or more pairwise cutoffs are too short to use with the specified rRESPA cutoffs.

*Pair style hybrid cannot have hybrid as an argument*

Self-explanatory. Check the input script.

*Pair style hybrid cannot use same pair style twice*

The sub-style arguments of pair\_style hybrid cannot be duplicated. Check the input script.

*Pair inner cutoff < Respa interior cutoff*

One or more pairwise cutoffs are too short to use with the specified rRESPA cutoffs.

*Pair inner cutoff >= Pair outer cutoff*

The specified cutoffs for the pair style are inconsistent.

*Pair style is incompatible with DihedralCharmm*

When using a dihedral style charmm, a pair style with a CHARMM component must also be selected, so that 1–4 pairwise coefficients are specified.

*Pair style is incompatible with KSpace style*

If a pair style with a long-range Coulombic component is selected, then a kspace style must also be used.

*Pair table cutoffs must all be equal to use with KSpace*

When using pair style table with a long-range KSpace solver, the cutoffs for all atom type pairs must all be the same, since the long-range solver starts at that cutoff.

*Pair\_coeff command before pair\_style is defined*

Self-explanatory.

*Pair\_coeff command before simulation box is defined*

The pair\_coeff command cannot be used before a read\_data, read\_restart, or create\_box command.

*Pair\_modify command before pair\_style is defined*

Self-explanatory.

*Pair\_write command before pair\_style is defined*

Self-explanatory.

*POEMS fix must come before NPT/NPH fix*

NPT/NPH fix must be defined in input script after all poems fixes, else the fix contribution to the pressure virial is incorrect.

*Potential with shear history requires newton pair off*

Granular potentials that include shear history effects can only be run with a newton setting where pairwise newton is "off".

*Proc grid in z != 1 for 2d simulation*

There cannot be more than 1 processor in the z dimension of a 2d simulation.

*Processor partitions are inconsistent*

The total number of processors in all partitions must match the number of processors LAMMPS is running on.

*Processors command after simulation box is defined*

The processors command cannot be used after a read\_data, read\_restart, or create\_box command.

*Quaternion creation numeric error*

A numeric error occurred in the creation of a rigid body by the fix rigid command.

*Quotes in a single arg*

A single word should not be quoted in the input script; only a set of words with intervening spaces should be quoted.

*R0 < 0 for fix spring command*

Equilibrium spring length is invalid.

*Region union region ID does not exist*

One or more of the region IDs specified by the region union command does not exist.

*Replacing a fix, but new style != old style*

A fix ID can be used a 2nd time, but only if the style matches the previous fix. In this case it is assumed you wish to reset a fix's parameters. This error may mean you are mistakenly re-using a fix ID when you do not intend to.

*Replicate command before simulation box is defined*

The replicate command cannot be used before a read\_data, read\_restart, or create\_box command.

*Replicate did not assign all atoms correctly*

Atoms replicated by the replicate command were not assigned correctly to processors. This is likely due to some atom coordinates being outside a non-periodic simulation box.

*Requested atom types in EAM setfl file do not exist*

Atom type specified in pair\_style eam command does not match number of types in setfl potential file.

*Respa inner cutoffs are invalid*

The first cutoff must be  $\leq$  the second cutoff.

*Respa inner/middle/outer used with invalid pair style*

Only a few pair potentials support the use of respa inner, middle, outer options.

*Respa levels must be  $\geq 1$*

Self-explanatory.

*Respa middle cutoffs are invalid*

The first cutoff must be  $\leq$  the second cutoff.

*Respa not allowed with atom style granular*

Respa cannot be used with the granular atom style.

*Reuse of dump ID*

A dump ID cannot be used twice.

*Reuse of region ID*

A region ID cannot be used twice.

*Reuse of temperature ID*

A temperature ID cannot be used twice.

*Rigid body has degenerate moment of inertia*

Fix poems will only work with bodies (collections of atoms) that have non-zero principal moments of inertia. This means they must be 3 or more non-collinear atoms, even with joint atoms removed.

*Rigid fix must come before NPT/NPH fix*

NPT/NPH fix must be defined in input script after all rigid fixes, else the rigid fix contribution to the pressure virial is incorrect.

*Run command before simulation box is defined*

The run command cannot be used before a read\_data, read\_restart, or create\_box command.

*Run\_style command before simulation box is defined*

The run\_style command cannot be used before a read\_data, read\_restart, or create\_box command.

*Set command before simulation box is defined*

The set command cannot be used before a read\_data, read\_restart, or create\_box command.

*Set command with no atoms existing*

No atoms are yet defined so the set command cannot be used.

*Shake angles have different bond types*

All 3-atom angle-constrained SHAKE clusters specified by the fix shake command that are the same angle type, must also have the same bond types for the 2 bonds in the angle.

*Shake atoms %d %d %d %d missing on proc %d at step %d*

The 4 atoms in a single shake cluster specified by the fix shake command are not all accessible to a processor. This probably means an atom has moved too far.

*Shake atoms %d %d %d missing on proc %d at step %d*

The 3 atoms in a single shake cluster specified by the fix shake command are not all accessible to a processor. This probably means an atom has moved too far.

*Shake atoms %d %d missing on proc %d at step %d*

The 2 atoms in a single shake cluster specified by the fix shake command are not all accessible to a processor. This probably means an atom has moved too far.

*Shake cluster of more than 4 atoms*



A single cluster specified by the fix shake command can have no more than 4 atoms.

*Shake clusters are connected*  
A single cluster specified by the fix shake command must have a single central atom with up to 3 other atoms bonded to it.

*Shake determinant = 0.0*  
The determinant of the matrix being solved for a single cluster specified by the fix shake command is numerically invalid.

*Shake fix must come before NPT/NPH fix*  
NPT fix must be defined in input script after SHAKE fix, else the SHAKE fix contribution to the pressure virial is incorrect.

*Substitution for undefined variable*  
The variable specified with a \$ symbol in an input script command has not been previously defined with a variable command.

*Temperature region ID does not exist*  
The region ID specified in the temperature command does not exist.

*Temper command before simulation box is defined*  
The temper command cannot be used before a read\_data, read\_restart, or create\_box command.

*Tempering fix ID is not defined*  
The fix ID specified by the temper command does not exist.

*Tempering fix is not valid*  
The fix specified by the temper command is not one that controls temperature (nvt or langevin).

*Thermodynamics not computed on tempering swap steps*  
The thermo command must insure that thermodynamics (including energy) is computed on the timesteps that tempering swaps are attempted.

*Thermodynamics must compute PE for temper*  
The thermo style must insure that thermodynamics computations include potential energy when tempering is performed.

*Thermo\_style command before simulation box is defined*  
The thermo\_style command cannot be used before a read\_data, read\_restart, or create\_box command.

*Timestep must be >= 0*  
Specified timestep size is invalid.

*TIP4P hydrogen has incorrect atom type*  
The TIP4P pairwise computation found an H atom whose type does not agree with the specified H type.

*TIP4P hydrogen is missing*  
The TIP4P pairwise computation failed to find the correct H atom within a water molecule.

*TMD target file did not list all group atoms*  
The target file for the fix tmd command did not list all atoms in the fix group.

*Too big a problem to run with a molecular atom style*  
Cannot run a problem with  $> 2^{31}$  atoms with molecular attributes.

*Too few bits for lookup table*  
Table size specified via pair\_modify command does not work with your machine's floating point representation.

*Too large an atom type in create\_atoms command*  
The atoms to be created by the create\_atoms command must have a valid type.

*Too many atoms in data file*  
A data file cannot contain more than  $2^{31}$  atoms.

*Too many atoms to use delete atoms command*  
Cannot use delete\_atoms command if number of atoms is greater than  $2^{31}$ .

*Too many atoms to use velocity create with loop all*

- Cannot use velocity create command with loop all setting if number of atoms is greater than  $2^{31}$ .  
Switch to local or geom setting.
- Too many exponent bits for lookup table*  
Table size specified via pair\_modify command does not work with your machine's floating point representation.
- Too many mantissa bits for lookup table*  
Table size specified via pair\_modify command does not work with your machine's floating point representation.
- Too many groups*  
The maximum number of atom groups (including the "all" group) is given by MAX\_GROUP in group.cpp and is 32.
- Too many masses for fix shake*  
The fix shake command cannot list more masses than there are atom types.
- Too many total bits for bitmapped lookup table*  
Table size specified via pair\_modify command is too large. Note that a value of N generates a  $2^N$  size table.
- Too many touching neighbors – boost MAXTOUCH*  
A granular simulation has too many neighbors touching one atom. The MAXTOUCH parameter in fix\_shear\_history.cpp must be set larger and LAMMPS must be re-built.
- Tree structure in joint connections*  
Fix poems cannot (yet) work with coupled bodies whose joints connect the bodies in a tree structure.
- Unbalanced quotes in input line*  
No matching end double quote was found following a leading double quote.
- Unexpected end of data file*  
LAMMPS hit the end of the data file while attempting to read a section. Something is wrong with the format of the data file.
- Units command after simulation box is defined*  
The units command cannot be used after a read\_data, read\_restart, or create\_box command.
- Unknown atom style in restart file*  
The atom style stored in the restart file is not recognized by LAMMPS.
- Unknown command: %s*  
The command is not known to LAMMPS. Check the input script.
- Unknown identifier in data file: %s*  
A section of the data file cannot be read by LAMMPS.
- Unknown section in data file: %s*  
The keyword for a section of the data file is not recognized by LAMMPS.
- Unknown table style in pair\_style command*  
Style of table is invalid for use with pair\_style table command.
- Universe variable count < # of partitions*  
A world-style variable must specify a number of values  $\geq$  to the number of processor partitions.
- Use of displace\_atoms with undefined lattice*  
Must use lattice command with displace\_atoms command if units option is set to lattice.
- Use of fix indent with undefined lattice*  
The lattice command must be used to define a lattice before using the fix indent command.
- Use of region with undefined lattice*  
If scale = lattice (the default) for the region command, then a lattice must first be defined via the lattice command.
- Use of temperature ramp with undefined lattice*  
If scale = lattice (the default) for the temperature ramp command, then a lattice must first be defined via the lattice command.
- Use of velocity with undefined lattice*

If scale = lattice (the default) for the velocity set or velocity ramp command, then a lattice must first be defined via the lattice command.

*Using variable equal keyword before simulation box is defined*

Cannot use simulation domain keywords in a equal style variable definition until the simulation box has been defined.

*Using variable equal keyword before initial run*

Cannot use thermodynamic keywords in a equal style variable definition until a simulation run has been performed.

*Velocity command before simulation box is defined*

The velocity command cannot be used before a read\_data, read\_restart, or create\_box command.

*Velocity command with no atoms existing*

A velocity command has been used, but no atoms yet exist.

*Velocity ramp in z for a 2d problem*

Self-explanatory.

*World variable count doesn't match # of partitions*

A world-style variable must specify a number of values equal to the number of processor partitions.

*Write\_restart command before simulation box is defined*

The write\_restart command cannot be used before a read\_data, read\_restart, or create\_box command.

## Warnings:

*FENE bond too long: %d %g*

A FENE bond has stretched dangerously far. It's interaction strength will be truncated to attempt to prevent the bond from blowing up.

*FENE bond too long: %d %d %d %g*

A FENE bond has stretched dangerously far. It's interaction strength will be truncated to attempt to prevent the bond from blowing up.

*Group for fix\_modify temp != fix group*

The fix\_modify command is specifying a temperature computation that computes a temperature on a different group of atoms than the fix itself operates on. This is probably not what you want to do.

*Less insertions than requested*

Less atom insertions occurred on this timestep due to the fix insert command than were scheduled. This is probably because there were too many overlaps detected.

*Lost atoms: original %.15g current %.15g*

A thermodynamic computation has detected lost atoms.

*Mismatch between velocity and temperature groups*

The temperature computation used by the velocity command will not be on the same group of atoms that velocities are being set for. This is probably not what you want.

*More than one dump custom with a centro attribute*

Each dump custom command that uses a per-atom centro attribute will cause a full neighbor list to be built and looped over. Thus it may be inefficient to use this attribute in multiple dump custom commands.

*More than one dump custom with a stress attribute*

Each dump custom command that uses a per-atom stress tensor attribute will cause the neighbor list to be looped over and inter-processor communication to be performed. Thus it may be inefficient to use these attributes in multiple dump custom commands.

*More than one dump custom with an energy attribute*

Each dump custom command that uses a per-atom energy attribute will cause the neighbor list to be looped over and inter-processor communication to be performed. Thus it may be inefficient to use this attribute in multiple dump custom commands.

*More than one msd fix*

- This will be computationally inefficient.
- More than one poems fix*  
This will be computationally inefficient and compute the fix's contribution to the virial (pressure) incorrectly.
- More than one rigid fix*  
This will be computationally inefficient and compute the fix's contribution to the virial (pressure) incorrectly.
- No fixes defined, atoms won't move*  
If you are not using a fix like nve, nvt, npt then atom velocities and coordinates will not be updated during timestepping.
- No joints between rigid bodies, use fix rigid instead*  
The bodies defined by fix poems are not connected by joints. POEMS will integrate the body motion, but it would be more efficient to use fix rigid.
- One or more respa levels compute no forces*  
This is computationally inefficient.
- Replacing a fix, but new group != old group*  
The ID and style of a fix match for a fix you are changing with a fix command, but the new group you are specifying does not match the old group.
- Replicating in a non-periodic dimension*  
The parameters for a replicate command will cause a non-periodic dimension to be replicated; this may cause unwanted behavior.
- Resetting angle\_style to restart file value*  
The angle style defined in the LAMMPS input script does not match that of the restart file.
- Resetting bond\_style to restart file value*  
The bond style defined in the LAMMPS input script does not match that of the restart file.
- Resetting boundary settings to restart file values*  
The boundary settings defined in the LAMMPS input script do not match that of the restart file.
- Resetting dihedral\_style to restart file value*  
The dihedral style defined in the LAMMPS input script does not match that of the restart file.
- Resetting dimension to restart file value*  
The dimension value defined in the LAMMPS input script does not match that of the restart file.
- Resetting improper\_style to restart file value*  
The improper style defined in the LAMMPS input script does not match that of the restart file.
- Resetting newton bond to restart file value*  
The value of the newton setting for bonds defined in the LAMMPS input script does not match that of the restart file.
- Resetting pair\_style to restart file value*  
The pair style defined in the LAMMPS input script does not match that of the restart file.
- Resetting reneighboring criteria during minimization*  
Minimization requires that neigh\_modify settings be delay = 0, every = 1, check = yes. Since these settings were not in place, LAMMPS changed them and will restore them to their original values after the minimization.
- Resetting unit\_style to restart file value*  
The unit style defined in the LAMMPS input script does not match that of the restart file.
- Restart file used different # of processors*  
The restart file was written out by a LAMMPS simulation running on a different number of processors. Due to round-off, the trajectories of your restarted simulation may diverge a little more quickly than if you ran on the same # of processors.
- Restart file used different 3d processor grid*  
The restart file was written out by a LAMMPS simulation running on a different 3d grid of processors. Due to round-off, the trajectories of your restarted simulation may diverge a little more

quickly than if you ran on the same # of processors.

*Restart file used different newton pair setting*

The restart file was written out by a LAMMPS simulation running with a different value of the newton pair setting. The new simulation will use the value from the input script.

*Restart file version does not match LAMMPS version*

The version of LAMMPS that wrote the restart file does not match the version of LAMMPS that is reading the restart file. Generally this shouldn't be a problem, since restart file formats won't change very often if at all. But if they do, the code will probably crash trying to read the file. Versions of LAMMPS are specified by a date.

*Shake determinant < 0.0*

The determinant of the quadratic equation being solved for a single cluster specified by the fix shake command is numerically suspect. LAMMPS will set it to 0.0 and continue.

*System is not charge neutral, net charge = %g*

The total charge on all atoms on the system is not 0.0, which is not valid for Ewald or PPPM.

*Table inner cutoff >= outer cutoff*

You specified an inner cutoff for a Coulombic table that is longer than the global cutoff. Probably not what you wanted.

*Temperature for NPH is not for group all*

User-assigned temperature to NPH fix does not compute temperature for all atoms. Since NPH computes a global pressure, the kinetic energy contribution from the temperature is assumed to also be for all atoms. Thus the pressure used by NPH could be inaccurate.

*Temperature for NPH is style region*

User-assigned temperature to NPH fix has style region. Since NPT computes a global pressure, the kinetic energy contribution from the temperature is assumed to also be for all atoms. Thus the pressure used by NPT could be inaccurate.

*Temperature for NPT is not for group all*

User-assigned temperature to NPT fix does not compute temperature for all atoms. Since NPT computes a global pressure, the kinetic energy contribution from the temperature is assumed to also be for all atoms. Thus the pressure used by NPT could be inaccurate.

*Temperature for NPT is style region*

User-assigned temperature to NPT fix has style region. Since NPT computes a global pressure, the kinetic energy contribution from the temperature is assumed to also be for all atoms. Thus the pressure used by NPT could be inaccurate.

*Temperature for NVT is style region*

User-assigned temperature to NVT fix has style region. Since NVT is a Nose/Hoover formulation that tracks average properties of a collection of atoms over time, it may be inaccurate to do this if the atoms in the region change.

*Temperature for temp/rescale is style region*

User-assigned temperature to temp/rescale fix has style region, but the temp/rescale fix did not specify a region. This means the temperature may be computed on a different set of atoms than are rescaled.

*Temperature for thermo pressure is not for group all*

User-assigned temperature to thermo via the thermo\_modify command does not compute temperature for all atoms. Since thermo computes a global pressure, the kinetic energy contribution from the temperature is assumed to also be for all atoms. Thus the pressure printed by thermo could be inaccurate.

*Temperature for thermo pressure is style region*

User-assigned temperature to thermo via the thermo\_modify command has style region. Since thermo computes a global pressure, the kinetic energy contribution from the temperature is assumed to also be for all atoms. Thus the pressure printed by thermo could be inaccurate.

*Using variable equal keyword with non-current thermo*

The variable expression is being evaluated with a thermodynamic quantity on a timestep when thermodynamic information may not be current.

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## 10. Future and history

This section lists features we are planning to add to LAMMPS, features of previous versions of LAMMPS, and features of other parallel molecular dynamics codes I've distributed.

### 10.1 [Coming attractions](#)

### 10.2 [Past versions](#)

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#### 10.1 Coming attractions

The current version of LAMMPS incorporates nearly all the features from previous parallel MD codes I developed. These include earlier versions of LAMMPS itself, Warp and ParaDyn for metals, and GranFlow for granular materials.

These are new features I'd like to eventually add to LAMMPS. Some are being worked on; some haven't been implemented because of lack of time or interest; others are just a lot of work!

- Monte Carlo bond-swapping for polymers (was in Fortran LAMMPS)
  - torsional shear boundary conditions and temperature calculation
  - bond creation potentials
  - point dipole force fields
  - 3-body force fields for materials like Si or silica
  - modified EAM (MEAM) potentials for metals
  - REAXX force field from Bill Goddard's group
  - pressure and energy tail corrections for pairwise interactions
  - Parinello-Rahman non-rectilinear simulation box
- 

#### 10.2 Past versions

LAMMPS development began in the mid 1990s under a cooperative research & development agreement (CRADA) between two DOE labs (Sandia and LLNL) and 3 companies (Cray, Bristol Myers Squibb, and Dupont). Soon after the CRADA ended, a final F77 version of the code, LAMMPS 99, was released. As development of LAMMPS continued at Sandia, the memory management in the code was converted to F90; a final F90 version was released as LAMMPS 2001.

The current LAMMPS is a rewrite in C++ and was first publicly released in 2004. It includes many new features, including features from other parallel molecular dynamics codes written at Sandia, namely ParaDyn, Warp, and GranFlow. ParaDyn is a parallel implementation of the popular serial DYNAMO code developed by Stephen Foiles and Murray Daw for their embedded atom method (EAM) metal potentials. ParaDyn uses atom- and force-decomposition algorithms to run in parallel. Warp is also a parallel implementation of the EAM potentials designed for large problems, with boundary conditions specific to shearing solids in varying geometries. GranFlow is a granular materials code with potentials and boundary conditions peculiar to granular systems. All of these codes (except ParaDyn) use spatial-decomposition techniques for their parallelism.

These older codes are available for download from the [LAMMPS WWW site](#), except for Warp & GranFlow which were primarily used internally. A brief listing of their features is given here.

#### LAMMPS 2001

- F90 + MPI
- dynamic memory
- spatial–decomposition parallelism
- NVE, NVT, NPT, NPH, rRESPA integrators
- LJ and Coulombic pairwise force fields
- all–atom, united–atom, bead–spring polymer force fields
- CHARMM–compatible force fields
- class 2 force fields
- 3d/2d Ewald & PPPM
- various force and temperature constraints
- SHAKE
- Hessian–free truncated–Newton minimizer
- user–defined diagnostics

#### LAMMPS 99

- F77 + MPI
- static memory allocation
- spatial–decomposition parallelism
- most of the LAMMPS 2001 features with a few exceptions
- no 2d Ewald & PPPM
- molecular force fields are missing a few CHARMM terms
- no SHAKE

#### Warp

- F90 + MPI
- spatial–decomposition parallelism
- embedded atom method (EAM) metal potentials + LJ
- lattice and grain–boundary atom creation
- NVE, NVT integrators
- boundary conditions for applying shear stresses
- temperature controls for actively sheared systems
- per–atom energy and centro–symmetry computation and output

#### ParaDyn

- F77 + MPI
- atom– and force–decomposition parallelism
- embedded atom method (EAM) metal potentials
- lattice atom creation
- NVE, NVT, NPT integrators
- all serial DYNAMO features for controls and constraints

#### GranFlow

- F90 + MPI
- spatial-decomposition parallelism
- frictional granular potentials
- NVE integrator
- boundary conditions for granular flow and packing and walls
- particle insertion

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---

## angle\_coeff command

### Syntax:

```
angle_coeff N args
```

- N = angle type (see asterik form below)
- args = coefficients for one or more angle types

### Examples:

```
angle_coeff 1 300.0 107.0
angle_coeff * 5.0
angle_coeff 2*10 5.0
```

### Description:

Specify the force field coefficients for one or more angle types. The number and meaning of the coefficients depends on the angle style. As described below, angle coefficients can also be set in the data file read by the [read\\_data](#) command or in a restart file.

N can be specified in one of two ways. An explicit numeric value can be used, as in the 1st example above. Or a wild-card asterik can be used to set the coefficients for multiple angle types. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If N = the number of angle types, then an asterik with no numeric values means all types from 1 to N. A leading asterik means all types from 1 to n (inclusive). A trailing asterik means all types from n to N (inclusive). A middle asterik means all types from m to n (inclusive).

Note that using 2 angle\_coeff commands for the same angle type is perfectly valid. For example, these commands set the coeffs for all angle types, then overwrite the coeffs for just angle type 2:

```
angle_coeff * 200.0 107.0 1.2
angle_coeff 2 50.0 107.0
```

A line in a data file that specifies angle coefficients uses the exact same format as the arguments of the angle\_coeff command in an input script, except that wild-card asteriks should not be used since coefficients for all N types are listed in the file. For example, under the "Angle Coeffs" section of a data file, the line that corresponds to the 1st example above would be listed as

```
1 300.0 107.0
```

The [units](#) of each coefficient are shown in parenthesis.

---



$$E = K(\theta - \theta_0)^2 + K_{UB}(r - r_{UB})^2$$

For style *charmm*, specify 4 coefficients:

- K (energy/radian^2)
- theta0 (degrees)
- K\_ub (energy/distance^2)
- r\_ub (distance)

Theta0 is specified in degrees, but LAMMPS converts it to radians internally; hence the units of K are in energy/radian^2.

$$\begin{aligned} E &= E_a + E_{bb} + E_{ba} \\ E_a &= K_2(\theta - \theta_0)^2 + K_3(\theta - \theta_0)^3 + K_4(\theta - \theta_0)^4 \\ E_{bb} &= M(r_{ij} - r_1)(r_{jk} - r_2) \\ E_{ba} &= N_1(r_{ij} - r_1)(\theta - \theta_0) + N_2(r_{jk} - r_2)(\theta - \theta_0) \end{aligned}$$

For style *class2*, only coefficients for the  $E_a$  formula can be specified in the input script. These are the 4 coefficients:

- theta0 (degrees)
- K2 (energy/radian^2)
- K3 (energy/radian^2)
- K4 (energy/radian^2)

Theta0 is specified in degrees, but LAMMPS converts it to radians internally; hence the units of K are in energy/radian^2.

Coefficients for the  $E_{bb}$  and  $E_{ba}$  formulas must be specified in the data file.

For the  $E_{bb}$  formula, the coefficients are listed under a "BondBond Coeffs" heading and each line lists 3 coefficients:

- M (energy/distance^2)
- r1 (distance)
- r2 (distance)

For the  $E_{ba}$  formula, the coefficients are listed under a "BondAngle Coeffs" heading and each line lists 4 coefficients:

- N1 (energy/distance^2)
- N2 (energy/distance^2)
- r1 (distance)
- r2 (distance)

The theta0 value in the  $E_{ba}$  formula is not specified, since it is the same value from the  $E_a$  formula.

$$E = K[1 + \cos(\theta)]$$

For style *cosine*, specify 1 coefficient:

- K (energy)

$$E = K[\cos(\theta) - \cos(\theta_0)]^2$$

For style *cosine/squared*, specify 2 coefficients:

- K (energy)
- theta0 (degrees)

Theta0 is specified in degrees, but LAMMPS converts it to radians internally.

$$E = K(\theta - \theta_0)^2$$

For style *harmonic*, specify 2 coefficients:

- K (energy/radian^2)
- theta0 (degrees)

Theta0 is specified in degrees, but LAMMPS converts it to radians internally; hence the units of K are in energy/radian^2.

For style *hybrid*, the first coefficient sets the angle style and the remaining coefficients are those appropriate to that style. For example, these commands:

```
angle_coeff 1 cosine 30.0
angle_coeff 2 harmonic 80.0 120.0
```

would set bonds of angle type 1 to be computed with a *cosine* potential. Likewise, angles of angle type 2 would be computed with a *harmonic* potential.

### Restrictions:

This command must come after the simulation box is defined by a read\_data, read\_restart, or create\_box command.

An angle style must be defined before any angle coefficients are set, either in the input script or in a data file.

### Related commands:

angle\_style

**Default:** none

angle\_coeff command

## angle\_style command

### Syntax:

```
angle_style style
```

- style = *none* or *charmm* or *class2* or *cosine* or *cosine/squared* or *harmonic* or *hybrid*

### Examples:

```
angle_style harmonic
angle_style charmm
angle_style hybrid harmonic cosine
```

### Description:

Set the formula(s) LAMMPS will use to compute angle interactions between triplets of atoms. The list of atom triplets is specified in the data or restart file and is read in by a [read\\_data](#) or [read\\_restart](#) command. The coefficients for the formula for each angle type can also be specified in those files or via the [angle\\_coeff](#) command. In all the formulas to follow, *theta* is the angle defined by the triplet of atoms.

A style of *none* means angle forces are not computed, even if angles are defined.

---

The *charmm* style uses the potential

$$E = K(\theta - \theta_0)^2 + K_{UB}(r - r_{UB})^2$$

with an additional Urey-Bradley term based on the distance *r* between the 1st and 3rd atoms in the angle. K, theta0, Kub, and Rub are coefficients defined for each angle type.

---

The *class2* style uses the potential

$$\begin{aligned} E &= E_a + E_{bb} + E_{ba} \\ E_a &= K_2(\theta - \theta_0)^2 + K_3(\theta - \theta_0)^3 + K_4(\theta - \theta_0)^4 \\ E_{bb} &= M(r_{ij} - r_1)(r_{jk} - r_2) \\ E_{ba} &= N_1(r_{ij} - r_1)(\theta - \theta_0) + N_2(r_{jk} - r_2)(\theta - \theta_0) \end{aligned}$$

where *E<sub>a</sub>* is the angle term, *E<sub>bb</sub>* is a bond–bond term, and *E<sub>ba</sub>* is a bond–angle term. Theta0 is the equilibrium angle and r1 and r2 are the equilibrium bond lengths. Kn, M, Nn, theta0, r1, r2 are coefficients defined for each angle type.

---

The *cosine* style uses the potential

$$E = K[1 + \cos(\theta)]$$

where K is defined for each angle type.

---

The *cosine/squared* style is a potential commonly used in the Gromacs MD code and is of the form

$$E = K[\cos(\theta) - \cos(\theta_0)]^2$$

where theta0 is the equilibrium value of the angle, and K is a prefactor. Note that the usual 1/2 factor is included in K. K and theta0 are coefficients defined for each angle type.

---

The *harmonic* style uses the potential

$$E = K(\theta - \theta_0)^2$$

where theta0 is the equilibrium value of the angle, and K is a prefactor. Note that the usual 1/2 factor is included in K. K and theta0 are coefficients defined for each angle type.

---

The *hybrid* style enables the use of multiple angle styles in one simulation. An angle style is assigned to each angle type. For example, angles in a polymer flow (of angle type 1) could be computed with a *cosine* potential and angles in the wall boundary (of angle type 2) could be computed with a *harmonic* potential. The assignment of angle type to style is made via the angle coeff command or in the data file.

---

### Restrictions:

Angle styles can only be set for atom\_styles that allow angles to be defined.

Angle styles are part of the "molecular" package. They are only enabled if LAMMPS was built with that package. See the Making LAMMPS section for more info.

### Related commands:

angle coeff

### Default:

angle\_style none

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---

## atom\_modify command

### Syntax:

atom\_modify keyword value ...

atom\_modify command

- one or more keyword/value pairs may be appended
- keyword = *map*

*map* value = *array* or *hash*

### Examples:

```
atom_modify map hash
```

### Description:

Modify properties of the atom style selected within LAMMPS.

The *map* keyword determines how atom ID lookup is done for molecular problems. Lookups are performed by bond (angle, etc) routines in LAMMPS to find the local atom index associated with a global atom ID. When the *array* value is used, each processor stores a lookup table of length N, where N is the total # of atoms in the system. This is the fastest method for most simulations, but a processor can run out of memory to store the table for very large simulations. The *hash* value uses a hash table to perform the lookups. This method can be slightly slower than the *array* method, but its memory cost is proportional to N/P on each processor, where P is the total number of processors running the simulation.

### Restrictions:

This command must be used before the simulation box is defined by a [read\\_data](#) or [create\\_box](#) command.

**Related commands:** none

### Default:

By default, atomic (non-molecular) problems do not allocate maps. For molecular problems, the option default is map = array.

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---

## atom\_style command

### Syntax:

```
atom_style style args
```

- style = *angle* or *atomic* or *bond* or *charge* or *dipole* or *dpd* or *full* or *granular* or *molecular* or *hybrid*

args = none for any style except *hybrid*  
*hybrid* args = list of one or more styles

### Examples:

```
atom_style bond
atom_style full
atom_style hybrid charge bond
```

### Description:

atom\_style command

Define what style of atoms to use in a simulation. This determines what attributes are associated with the atoms. This command must be used before a simulation is setup via a [read\\_data](#), [read\\_restart](#), or [create\\_box](#) command.

Once a style is assigned, it cannot be changed, so use a style general enough to encompass all attributes. E.g. with style *bond*, angular terms cannot be used or added later to the model. It is OK to use a style more general than needed, though it may be slightly inefficient.

The choice of style affects what quantities are stored by each atom, what quantities are communicated between processors to enable forces to be computed, and what quantities are listed in the data file read by the [read\\_data](#) command.

These are the attributes of each style. All styles store coordinates, velocities, atom IDs and types.

- *angle* = bonds and angles – e.g. bead–spring polymers with stiffness
- *atomic* = only the default values
- *bond* = bonds – e.g. bead–spring polymers
- *charge* = charge
- *dipole* = charge + dipole moments
- *dpd* = default values, also communicates velocities
- *molecular* = bonds, angles, dihedrals, impropers – e.g. all–atom polymers
- *full* = molecular + charge – e.g. biomolecules, charged polymers
- *granular* = granular material with rotational properties

Typical simulations with a single pair potential will use only one of these styles. For cases where multiple pair potentials will be used (see the [pair\\_style hybrid](#) command), it may be necessary to use multiple atom styles. Another example is doing a DPD simulations with bonds or angles. In these cases the *hybrid* style can be used to list multiple atom styles. Atoms will then store and communicate the union of all quantities implied by the individual styles.

LAMMPS can be extended with new atom styles; see [this section](#).

### Restrictions:

This command cannot be used after the simulation box is defined by a [read\\_data](#) or [create\\_box](#) command.

The *angle*, *bond*, *full*, and *molecular* styles are part of the "molecular" package. The *granular* style is part of the "granular" package. The *dpd* style is part of the "dpd" package. They are only enabled if LAMMPS was built with that package. See the [Making LAMMPS](#) section for more info.

### Related commands:

[read\\_data](#), [pair\\_style](#)

**Default:** none

---

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---

## bond\_coeff command

### Syntax:

```
bond_coeff N args
```

- N = bond type (see asterik form below)
- args = coefficients for one or more bond types

### Examples:

```
bond_coeff 5 80.0 1.2
bond_coeff * 30.0 1.5 1.0 1.0
bond_coeff 1*4 30.0 1.5 1.0 1.0
bond_coeff 1 harmonic 200.0 1.0
```

### Description:

Specify the force field coefficients for one or more bond types. The number and meaning of the coefficients depends on the bond style. As described below, bond coefficients can also be set in the data file read by the read\_data command or in a restart file.

N can be specified in one of two ways. An explicit numeric value can be used, as in the 1st example above. Or a wild-card asterik can be used to set the coefficients for multiple bond types. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If N = the number of bond types, then an asterik with no numeric values means all types from 1 to N. A leading asterik means all types from 1 to n (inclusive). A trailing asterik means all types from n to N (inclusive). A middle asterik means all types from m to n (inclusive).

Note that using 2 bond\_coeff commands for the same bond type is perfectly valid. For example, these commands set the coeffs for all bond types, then overwrite the coeffs for just bond type 2:

```
bond_coeff * 100.0 1.2
bond_coeff 2 200.0 1.2
```

A line in a data file that specifies bond coefficients uses the exact same format as the arguments of the bond\_coeff command in an input script, except that wild-card asteriks should not be used since coefficients for all N types must be listed in the file. For example, under the "Bond Coeffs" section of a data file, the line that corresponds to the 1st example above would be listed as

```
5 80.0 1.2
```

The units of each coefficient are shown in parenthesis.

---

$$E = K_2(r - r_0)^2 + K_3(r - r_0)^3 + K_4(r - r_0)^4$$

For style *class2*, specify 4 coefficients:

- R0 (distance)
- K2 (energy/distance^2)
- K3 (energy/distance^2)

- K4 (energy/distance^2)
- 

$$E = -0.5K R_0^2 \ln \left[ 1 - \left( \frac{r}{R_0} \right)^2 \right] + 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] + \epsilon$$

For style *fene*, specify 4 coefficients:

- K (energy/distance^2)
  - R0 (distance)
  - epsilon (energy)
  - sigma (distance)
- 

$$E = -0.5K R_0 \ln \left[ 1 - \left( \frac{(r - \Delta)}{R_0} \right)^2 \right] + 4\epsilon \left[ \left( \frac{\sigma}{(r - \Delta)} \right)^{12} - \left( \frac{\sigma}{(r - \Delta)} \right)^6 \right] + \epsilon$$

For style *fene/expand*, specify 5 coefficients:

- K (energy/distance^2)
  - R0 (distance)
  - epsilon (energy)
  - sigma (distance)
  - delta (distance)
- 

$$E = K(r - r_0)^2$$

For style *harmonic*, specify 2 coefficients:

- K (energy/distance^2)
  - r0 (distance)
- 

$$E = D \left[ 1 - e^{-\alpha(r-r_0)} \right]^2$$

For style *morse*, specify 3 coefficients:

- D (energy)
  - alpha (inverse distance)
  - r0 (distance)
- 

$$E = \frac{\epsilon(r - r_0)^2}{[\lambda^2 - (r - r_0)^2]}$$



For style *nonlinear*, specify 3 coefficients:

- epsilon (energy)
  - r0 (distance)
  - lamda (distance)
- 

$$E = K(r - R_c)^2(r - R_c - B_1)(r - R_c - B_2) + U_0 + 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] + \epsilon$$

For style *quartic*, specify 5 coefficients:

- K (energy/distance^2)
- B1 (distance)
- B2 (distance)
- Rc (distance)
- U0 (energy)

Values of these coefficients that are tuned for coarse-grain polymer chains (bead-spring models) are discussed in the [bond\\_style](#) command documentation.

---

For style *hybrid*, the first coefficient sets the bond style and the remaining coefficients are those appropriate to that style. For example, these commands:

```
bond_coeff 1 fene 30.0 1.5 1.0 1.0
bond_coeff 2 harmonic 80.0 1.2
```

would set bonds of bond type 1 to be computed with a *fene* potential with coefficients 30.0, 1.5, 1.0, 1.0 for K, R0, epsilon, sigma. Likewise, bonds of bond type 2 would be computed with a *harmonic* potential with coefficients 80.0, 1.2 for K, r0.

---

### Restrictions:

This command must come after the simulation box is defined by a [read\\_data](#), [read\\_restart](#), or [create\\_box](#) command.

A bond style must be defined before any bond coefficients are set, either in the input script or in a data file.

### Related commands:

[bond\\_style](#)

**Default:** none

---

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---

## bond\_style command

### Syntax:

`bond_style style args`

- `style = none` or `class2` or `fene` or `fene/expand` or `harmonic` or `morse` or `nonlinear` or `quartic` or `hybrid`

`args = none` for any style except `hybrid`  
`hybrid args = list of one or more styles`

### Examples:

```
bond_style harmonic
bond_style fene
bond_style hybrid harmonic fene
```

### Description:

Set the formula(s) LAMMPS will use to compute bond interactions between pairs of atoms. The list of atom pairs is specified in the data or restart file and is read in by a `read_data` or `read_restart` command. The coefficients for the formula for each bond type can also be specified in those files or via the `bond_coeff` command. In all the formulas to follow,  $r$  is the distance between the 2 atoms in the bond.

A style of *none* means bond forces are not computed, even if bond are defined.

---

The *class2* style uses the potential

$$E = K_2(r - r_0)^2 + K_3(r - r_0)^3 + K_4(r - r_0)^4$$

where  $r_0$  is the equilibrium bond distance.  $K_n$  and  $r_0$  are coefficients defined for each bond type.

---

The *fene* style uses the potential

$$E = -0.5KR_0^2 \ln \left[ 1 - \left( \frac{r}{R_0} \right)^2 \right] + 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] + \epsilon$$

to define a finite extensible nonlinear elastic (FENE) potential (Kremer), used for bead-spring polymer models. The first term is attractive, the 2nd Lennard-Jones term is repulsive. The first term extends to  $R_0$ , the maximum extent of the bond. The 2nd term is cutoff at  $2^{1/6}$  sigma, the minimum of the LJ potential.  $K$ ,  $R_0$ , epsilon, and sigma are coefficients defined for each bond type.

---

The *fene/expand* style is similar to *fene* except that an extra shift factor of delta (positive or negative) is added to  $r$  to effectively change the bead size of the bonded atoms. The corresponding potential is

$$E = -0.5K R_0 \ln \left[ 1 - \left( \frac{(r - \Delta)}{R_0} \right)^2 \right] + 4\epsilon \left[ \left( \frac{\sigma}{(r - \Delta)} \right)^{12} - \left( \frac{\sigma}{(r - \Delta)} \right)^6 \right] + \epsilon$$

The first term now extends to  $R_0 + \Delta$  and the 2nd term is cutoff at  $2^{1/6} \sigma + \Delta$ . K,  $R_0$ , epsilon, sigma, and delta are coefficients defined for each bond type.

---

The *harmonic* style uses the potential

$$E = K(r - r_0)^2$$

where  $r_0$  is the equilibrium bond distance. Note that the usual 1/2 factor is included in K. K and  $r_0$  are coefficients defined for each bond type.

---

The *morse* style uses the potential

$$E = D \left[ 1 - e^{-\alpha(r-r_0)} \right]^2$$

where  $r_0$  is the equilibrium bond distance, alpha is a stiffness parameter, and D determines the depth of the potential well. D, alpha, and  $r_0$  are coefficients defined for each bond type.

---

The *nonlinear* style uses the potential

$$E = \frac{\epsilon(r - r_0)^2}{[\lambda^2 - (r - r_0)^2]}$$

to define an anharmonic spring (Rector) of equilibrium length  $r_0$  and maximum extension lamda. Epsilon,  $r_0$ , and lamda are coefficients defined for each bond type.

---

The *quartic* style uses the potential

$$E = K(r - R_c)^2(r - R_c - B_1)(r - R_c - B_2) + U_0 + 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] + \epsilon$$

to define a bond that can be broken as the simulation proceeds (e.g. due to a polymer being stretched). The sigma and epsilon used in the LJ portion of the formula are both set equal to 1.0 by LAMMPS. K, B1, B2,  $R_c$ , and  $U_0$  are coefficients defined for each bond type.

---

This potential was constructed to mimic the FENE bond potential for coarse-grained polymer chains. When monomers with sigma = epsilon = 1.0 are used, the following choice of parameters gives a quartic potential that looks nearly like the FENE potential: K = 1200, B1 = -0.55, B2 = 0.25,  $R_c$  = 1.3, and  $U_0$  = 34.6878. Different parameters can be specified using the bond coeff command, but you will need to choose them carefully so they form a suitable bond potential.

$R_c$  is the cutoff length at which the bond potential goes smoothly to a local maximum. If a bond length ever becomes  $> R_c$ , LAMMPS "breaks" the bond, which means two things. First, the bond potential is turned off by setting its type to 0, and is no longer computed. Second, a pairwise interaction between the two atoms is turned on, since they are no longer bonded.

LAMMPS does the second task via a computational sleight-of-hand. It subtracts the pairwise interaction as part of the bond computation. When the bond breaks, the subtraction stops. For this to work, the pairwise interaction must always be computed by the pair\_style command, whether the bond is broken or not. This means that special\_bonds must be set to 1,1,1, as indicated as a restriction below.

Note that when bonds are dumped to a file via dump bond, bonds with type 0 are not included. The delete\_bonds command can also be used to query the status of broken bonds or permanently delete them, e.g.:

```
delete_bonds all stats
delete_bonds all bond 0 remove
```

---

The *hybrid* style enables the use of multiple bond styles in one simulation. A bond style is assigned to each bond type. For example, bonds in a polymer flow (of bond type 1) could be computed with a *fene* potential and bonds in the wall boundary (of bond type 2) could be computed with a *harmonic* potential. The assignment of bond type to style is made via the bond\_coeff command or in the data file.

---

### Restrictions:

Bond styles can only be set for atom styles that allow bonds to be defined.

The *quartic* style requires that special\_bonds parameters be set to 1,1,1. Three- and four-body interactions (angle, dihedral, etc) cannot be used with *quartic* bonds.

Bond styles are part of the "molecular" package. They are only enabled if LAMMPS was built with that package. See the Making LAMMPS section for more info.

### Related commands:

bond\_coeff, delete\_bonds

### Default:

bond\_style none

---

**(Kremer)** Kremer, Grest, J Chem Phys, 92, 5057 (1990).

**(Rector)** Rector, Van Swol, Henderson, Molecular Physics, 82, 1009 (1994).

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## boundary command

### Syntax:

boundary x y z

- x,y,z = *p* or *s* or *f* or *m*, one or two letters

*p* is periodic  
*f* is non-periodic and fixed  
*s* is non-periodic and shrink-wrapped  
*m* is non-periodic and shrink-wrapped with a minimum value

### Examples:

```
boundary p p f
boundary p fs p
boundary s f fm
```

### Description:

Set the style of boundaries for the global simulation box in each dimension. A single letter assigns the same style to both the lower and upper face of the box. Two letters assigns the first style to the lower face and the second style to the upper face. The initial size of the simulation box is set by the [read\\_data](#), [read\\_restart](#), or [create\\_box](#) commands.

The style *p* means the box is periodic, so that particles interact across the boundary, and they can exit one end of the box and re-enter the other end. A periodic dimension can change in size due to constant pressure boundary conditions or volume rescaling (see the [fix\\_npt](#) and [fix\\_volume/rescale](#) commands). The *p* style must be applied to both faces of a dimension.

The styles *f*, *s*, and *m* mean the box is non-periodic, so that particles do not interact across the boundary and do not move from one side of the box to the other. For style *f*, the position of the face is fixed. If an atom moves outside the face it may be lost. For style *s*, the position of the face is set so as to encompass the atoms in that dimension (shrink-wrapping), no matter how far they move. For style *m*, shrink-wrapping occurs, but is bounded by the value specified in the data or restart file or set by the [create\\_box](#) command. For example, if the upper z face has a value of 50.0 in the data file, the face will always be positioned at 50.0 or above, even if the maximum z-extent of all the atoms becomes less than 50.0.

### Restrictions:

This command cannot be used after the simulation box is defined by a [read\\_data](#) or [create\\_box](#) command.

### Related commands:

See the [thermo\\_modify](#) command for a discussion of lost atoms.

### Default:

```
boundary p p p
```

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---

## cd command

### Syntax:

```
cd dir
```

- dir = directory to change to

### Examples:

```
cd subl  
cd ../new2  
cd ..
```

### Description:

Change the working directory. All subsequent LAMMPS commands that access files for reading or writing will use the new directory.

### Restrictions:

If the specified directory does not exist, LAMMPS will not detect the error.

**Related commands:** none

**Default:** none

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---

## clear command

### Syntax:

```
clear
```

### Examples:

```
(commands for 1st simulation)  
clear  
(commands for 2nd simulation)
```

### Description:

This command deletes all atoms, restores all settings to their default values, and frees all memory allocated by LAMMPS. Once a clear command has been executed, it is as if LAMMPS were starting over, with only the exceptions noted below. This command enables multiple jobs to be run sequentially from one input script.

These settings are not affected by a clear command: the working directory ([cd](#) command), log file status ([log](#) command), echo status ([echo](#) command), and input script variables ([variable](#) command).

**Restrictions:** none

**Related commands:** none

**Default:** none

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---

## create\_atoms command

### Syntax:

```
create_atoms type region-ID
```

- type = atom type (1–N) of atoms to create on a lattice
- region-ID = ID of region each atom will belong to (optional)

### Examples:

```
create_atoms 1 regsphere  
create_atoms 3
```

### Description:

This command creates atoms on a lattice as an alternative to reading in their coordinates via a [read\\_data](#) or [read\\_restart](#) command. A simulation box must already exist, which is created with the [create\\_box](#) command.

Before using this command, a lattice must be defined using the [lattice](#) command. If a region is not specified, the `create_atoms` command fills the entire simulation box with atoms on the lattice. If a region is specified, then the geometric volume is filled that is inside the simulation box and is also consistent with the region volume.

The `create_atoms` command can be used multiple times with different lattice orientations to create grain boundaries. Used in conjunction with the [delete\\_atoms](#) command, reasonably complex geometries can be created. The `create_atoms` command can also be used to add atoms to a system previously read in from a data or restart file. In all these cases, care should be taken to insure that new atoms do not overlap existing atoms inappropriately.

Created atoms are assigned the specified atom type and a velocity of 0.0.

### Restrictions:

An [atom\\_style](#) and [lattice](#) must be previously defined to use this command.

### Related commands:

[lattice](#), [orient](#), [origin](#), [region](#), [create\\_box](#), [read\\_data](#), [read\\_restart](#)

**Default:** none

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---

## create\_box command

### Syntax:

```
create_box N region-ID
```

- N = # of atom types to use in this simulation
- region-ID = ID of region to use as simulation domain

### Examples:

```
create_atoms 2 mybox
```

### Description:

This command creates a simulation box that encloses the specified region. Thus a region command must first be used to define a geometric domain. If the region is not of style *block*, LAMMPS encloses it with a rectangular simulation box.

The argument N is the number of atom types that will be used in the simulation.

### Restrictions:

An atom\_style and region must have been previously defined to use this command.

### Related commands:

create\_atoms, region

**Default:** none

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---

## delete\_atoms command

### Syntax:

```
delete_atoms style args
```

- style = *group* or *region* or *overlap*

```
group args = group-ID
```

```
region args = region-ID
```

```
overlap args = distance type1 type2
```

```
distance = delete atoms with neighbors within this cutoff (distance units)
```

```
type1 = type of first atom in pair (optional)
```

```
type2 = type of other atom in pair (optional)
```

### Examples:

create\_box command



```
delete_atoms group edge
delete_atoms region sphere
delete_atoms overlap 0.3
delete_atoms overlap 0.3 1 1
```

### Description:

Delete the specified atoms. This command can be used to carve out voids from a block of material or to delete created atoms that are too close to each other (e.g. at a grain boundary).

For style *group*, all atoms belonging to the group are deleted.

For style *region*, all atoms in the region volume are deleted.

For style *overlap*, pairs of atoms within the specified cutoff distance are searched for, and one of the 2 atoms is deleted. If no atom types are specified, an atom will always be deleted if the cutoff criterion is met. If a single atom type is specified, then one or both of the atoms in the pair must be of the specified type for a deletion to occur. If two atom types are specified, the two atoms in the pair must be of the specified types for a deletion to occur. For a given configuration of atoms, the only guarantee is that at the end of the deletion operation, enough deletions will have occurred that no atom pairs within the cutoff (and with the specified types) will remain. There is no guarantee that the minimum number of atoms will be deleted, or that the same atoms will be deleted when running on different numbers of processors.

After atoms are deleted, if the system is not molecular (no bonds), then atom IDs are re-assigned so that they run from 1 to the number of atoms in the system. This is not done for molecular systems, since it would foul up the bond connectivity that has already been assigned.

### Restrictions:

The *overlap* style requires inter-processor communication to acquire ghost atoms and setup a neighbor list. This means that your system must be ready to perform a simulation before using this command (force fields setup, atom masses set, etc).

If the [special\\_bonds](#) command is used with a setting of 0, then a pair of bonded atoms (1-2, 1-3, or 1-4) will not appear in the neighbor list, and thus will not be considered for deletion by the *overlap* style. You probably don't want to be deleting one atom in a bonded pair anyway.

### Related commands:

[create\\_atoms](#)

**Default:** none

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---

## delete\_bonds command

### Syntax:

```
delete_bonds group-ID style args keyword ...
```

- group-ID = group ID
- style = *multi* or *atom* or *bond* or *angle* or *dihedral* or *improper* or *stats*

```
multi args = none
atom args = an atom type
bond args = a bond type
angle args = an angle type
dihedral args = a dihedral type
improper args = an improper type
stats args = none
```

- zero or more keywords may be appended to the args
- keyword = *undo* or *remove* or *special*

### Examples:

```
delete_bonds frozen multi remove
delete_bonds all atom 4 special
delete_bonds all stats
```

### Description:

Turn off (or on) molecular topology interactions, i.e. bonds, angles, dihedrals, impropers. This command is useful for deleting interactions that have been previously turned off by bond-breaking potentials. It is also useful for turning off topology interactions between frozen or rigid atoms. Pairwise interactions can be turned off via the neigh\_modify exclude command. The fix shake command also effectively turns off certain bond and angle interactions.

For all styles, an interaction is only turned off (or on) if all the atoms involved are in the specified group. For style *multi* this is the only criterion applied – all types of bonds, angles, dihedrals, impropers in the group turned off.

For style *atom*, one or more of the atoms involved must also be of the specified type. For style *bond*, only bonds are candidates for turn-off, and the bond must be of the specified type. Styles *angle*, *dihedral*, and *improper* are treated similarly.

For style *bond*, you can set the type to 0 to delete bonds that have been previously broken; e.g. see the bond\_style quartic command.

For style *stats* no interactions are turned off (or on); the status of all interactions in the specified group is simply reported. This is useful for diagnostic purposes if bonds have been turned off by a bond-breaking potential during a previous run.

The default behavior of the `delete_bonds` command is to turn off interactions by toggling their type to a negative value. E.g. a `bond_type` of 2 is set to -2. The neighbor list creation routines will not include such an interaction in their interaction lists. The default is also to not alter the list of 1-2, 1-3, 1-4 neighbors computed by the special\_bonds command and used to weight pairwise force and energy calculations. This means that pairwise computations will proceed as if the bond (or angle, etc) were still turned on.

The keywords listed above can be appended to the argument list to alter the default behavior.

The *undo* keyword inverts the `delete_bonds` command so that the specified bonds, angles, etc are turned on if they are currently turned off. This means any negative value is toggled to positive. Note that the fix shake command also sets bond and angle types negative, so this option should not be used on those interactions.

The *remove* keyword is invoked at the end of the `delete_bonds` operation. It causes turned-off bonds (angles, etc) to be removed from each atom's data structure and then adjusts the global bond (angle, etc) counts accordingly. Removal is a permanent change; removed bonds cannot be turned back on via the *undo* keyword. Removal does not alter the pairwise 1-2, 1-3, 1-4 weighting list.

The *special* keyword is invoked at the end of the `delete_bonds` operation, after (optional) removal. It re-computes the pairwise 1-2, 1-3, 1-4 weighting list. The weighting list computation treats turned-off bonds the same as turned-on. Thus, turned-off bonds must be removed if you wish to change the weighting list.

Note that the choice of *remove* and *special* options affects how 1-2, 1-3, 1-4 pairwise interactions will be computed across bonds that have been modified by the `delete_bonds` command.

### Restrictions:

This command requires inter-processor communication to coordinate the deleting of bonds. This means that your system must be ready to perform a simulation before using this command (force fields setup, atom masses set, etc).

If deleted bonds (angles, etc) are removed but the 1-2, 1-3, 1-4 weighting list is not recomputed, this can cause a later `fix shake` command to fail due to an atom's bonds being inconsistent with the weighting list. This should only happen if the group used in the `fix` command includes both atoms in the bond, in which case you probably should be recomputing the weighting list.

### Related commands:

`neigh_modify` `exclude`, `special_bonds`, `fix shake`

**Default:** none

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---

## dielectric command

### Syntax:

```
dielectric value
```

- value = dielectric constant

### Examples:

```
dielectric 2.0
```

### Description:

Set the dielectric constant for Coulombic interactions (pairwise and long-range) to this value. The constant is unitless, since it is used to reduce the strength of the interactions. The value is used in the denominator of the formulas for Coulombic interactions – e.g. a value of 4.0 reduces the Coulombic interactions to 25% of their default strength. See the `pair_style` command for more details.

**Restrictions:** none

**Related commands:**

pair\_style

**Default:**

dielectric 1.0

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---

## dihedral\_coeff command

**Syntax:**

```
dihedral_coeff N args
```

- N = dihedral type (see asterik form below)
- args = coefficients for one or more dihedral types

**Examples:**

```
dihedral_coeff 1 80.0 1 3  
dihedral_coeff * 80.0 1 3 0.5  
dihedral_coeff 2* 80.0 1 3 0.5
```

**Description:**

Specify the force field coefficients for one or more dihedral types. The number and meaning of the coefficients depends on the dihedral style. As described below, dihedral coefficients can also be set in the data file read by the read\_data command or in a restart file.

N can be specified in one of two ways. An explicit numeric value can be used, as in the 1st example above. Or a wild-card asterik can be used to set the coefficients for multiple dihedral types. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If N = the number of dihedral types, then an asterik with no numeric values means all types from 1 to N. A leading asterik means all types from 1 to n (inclusive). A trailing asterik means all types from n to N (inclusive). A middle asterik means all types from m to n (inclusive).

Note that using 2 dihedral\_coeff commands for the same dihedral type is perfectly valid. For example, these commands set the coeffs for all dihedral types, then overwrite the coeffs for just dihedral type 2:

```
dihedral_coeff * 80.0 1 3  
dihedral_coeff 2 200.0 1 3
```

A line in a data file that specifies dihedral coefficients uses the exact same format as the arguments of the dihedral\_coeff command in an input script, except that wild-card asteriks should not be used since coefficients for all N types are listed in the file. For example, under the "Dihedral Coeffs" section of a data file, the line that corresponds to the 1st example above would be listed as

```
1 80.0 1 3
```

See the dihedral style command for more discussion of the formulas that use these coefficients. The units of each coefficient are shown in parenthesis.

---

$$E = K[1 + \cos(n\phi + d)]$$

For style *charmm*, specify 4 coefficients:

- K (energy)
- n (integer >= 0)
- d (integer value of degrees)
- weighting factor (0.0 to 1.0)

The weighting factor is applied to pairwise interaction between the 1st and 4th atoms in the dihedral. Note that this weighting factor is unrelated to the weighting factor specified by the special bonds command which applies to all 1–4 interactions in the system. For CHARMM force fields, the latter should typically be set to 0.0, else the 1–4 interactions in a dihedral will be computed twice (once in the pair routine, and once by the charmm/dihedral routine).

---

$$\begin{aligned} E &= E_d + E_{mbt} + E_{ebt} + E_{at} + E_{aat} + E_{bb13} \\ E_d &= \sum_{n=1}^3 K_n [1 - \cos(n\phi - \phi_n)] \\ E_{mbt} &= (r_{jk} - r_2)[A_1 \cos(\phi) + A_2 \cos(2\phi) + A_3 \cos(3\phi)] \\ E_{ebt} &= (r_{ij} - r_1)[B_1 \cos(\phi) + B_2 \cos(2\phi) + B_3 \cos(3\phi)] + \\ &\quad (r_{kl} - r_3)[C_1 \cos(\phi) + C_2 \cos(2\phi) + C_3 \cos(3\phi)] \\ E_{at} &= (\theta_{ijk} - \theta_1)[D_1 \cos(\phi) + D_2 \cos(2\phi) + D_3 \cos(3\phi)] + \\ &\quad (\theta_{jkl} - \theta_2)[E_1 \cos(\phi) + E_2 \cos(2\phi) + E_3 \cos(3\phi)] \\ E_{aat} &= M(\theta_{ijk} - \theta_1)(\theta_{jkl} - \theta_2) \cos(\phi) \\ E_{bb13} &= N(r_{ij} - r_1)(r_{kl} - r_3) \end{aligned}$$

For style *class2*, only coefficients for the Ed formula can be specified in the input script. These are the 6 coefficients:

- K1 (energy)
- phi1 (degrees)
- K2 (energy)
- phi2 (degrees)
- K3 (energy)
- phi3 (degrees)

Coefficients for all the other formulas must be specified in the data file.

For the Embt formula, the coefficients are listed under a "MiddleBondTorsion Coeffs" heading and each line lists 4 coefficients:

- A1 (energy/distance)

- A2 (energy/distance)
- A3 (energy/distance)
- r2 (distance)

For the Eebt formula, the coefficients are listed under a "EndBondTorsion Coeffs" heading and each line lists 8 coefficients:

- B1 (energy/distance)
- B2 (energy/distance)
- B3 (energy/distance)
- C1 (energy/distance)
- C2 (energy/distance)
- C3 (energy/distance)
- r1 (distance)
- r3 (distance)

For the Eat formula, the coefficients are listed under a "AngleTorsion Coeffs" heading and each line lists 8 coefficients:

- D1 (energy/radian)
- D2 (energy/radian)
- D3 (energy/radian)
- E1 (energy/radian)
- E2 (energy/radian)
- E3 (energy/radian)
- theta1 (degrees)
- theta2 (degrees)

Theta1 and theta2 are specified in degrees, but LAMMPS converts them to radians internally; hence the units of D and E are in energy/radian.

For the Eaat formula, the coefficients are listed under a "AngleAngleTorsion Coeffs" heading and each line lists 3 coefficients:

- M (energy/radian^2)
- theta1 (degrees)
- theta2 (degrees)

Theta1 and theta2 are specified in degrees, but LAMMPS converts them to radians internally; hence the units of M are in energy/radian^2.

For the Ebb13 formula, the coefficients are listed under a "BondBond13 Coeffs" heading and each line lists 3 coefficients:

- N (energy/distance^2)
- r1 (distance)
- r3 (distance)

---


$$E = K[1 + d \cos(n\phi)]$$

For style *harmonic*, specify 3 coefficients:

- K (energy)
  - d (+1 or -1)
  - n (integer  $\geq 0$ )
- 

$$E = A[1 - \cos(\theta)] + B[1 + \cos(3\theta)] + C[1 + \cos(\theta + \frac{\pi}{4})]$$

For style *helix*, specify 3 coefficients:

- A (energy)
  - B (energy)
  - C (energy)
- 

$$E = \sum_{n=1,5} A_n \cos^{n-1}(\phi)$$

For style *multiharmonic*, specify 5 coefficients:

- A1 (energy)
  - A2 (energy)
  - A3 (energy)
  - A4 (energy)
  - A5 (energy)
- 

$$E = \frac{1}{2}K_1[1 + \cos(\phi)] + \frac{1}{2}K_2[1 - \cos(2\phi)] + \frac{1}{2}K_3[1 + \cos(3\phi)] + \frac{1}{2}K_4[1 - \cos(4\phi)]$$

For style *opls*, specify 4 coefficients:

- K1 (energy)
  - K2 (energy)
  - K3 (energy)
  - K4 (energy)
- 

For style *hybrid*, the first coefficient sets the dihedral style and the remaining coefficients are those appropriate to that style. For example, these commands:

```
dihedral_coeff 1 harmonic 6.0 1 3  
dihedral_coeff 2 helix 10 10 10
```

would set bonds of dihedral type 1 to be computed with a *harmonic* potential. Likewise, dihedrals of dihedral type 2 would be computed with a *helix* potential.

---

### Restrictions:

This command must come after the simulation box is defined by a [read\\_data](#), [read\\_restart](#), or [create\\_box](#) command.

An dihedral style must be defined before any dihedral coefficients are set, either in the input script or in a data file.

#### Related commands:

[dihedral\\_style](#)

**Default:** none

---

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---

## dihedral\_style command

### Syntax:

```
dihedral_style style
```

- style = *none* or *charmm* or *class2* or *harmonic* or *helix* or *multi/harmonic* or *opls* or *hybrid*

### Examples:

```
dihedral_style harmonic
dihedral_style multi/harmonic
dihedral_style hybrid harmonic charmm
```

### Description:

Set the formula(s) LAMMPS will use to compute dihedral interactions between quadruplets of atoms. The list of atom quadruplets is specified in the data or restart file and is read in by a [read\\_data](#) or [read\\_restart](#) command. The coefficients for the formula for each dihedral type can also be specified in those files or by the [dihedral\\_coeff](#) command. In all the formulas to follow, *phi* is the torsional angle defined by the quadruplet of atoms.

Here are some important points to take note of when defining the LAMMPS dihedral coefficients in the formulas that follow so that they are compatible with other force fields:

- The LAMMPS convention is that the trans position = 180 degrees, while in some force fields trans = 0 degrees.
- Some force fields reverse the sign convention on *d*.
- Some force fields divide/multiply *K* by the number of multiple torsions that contain the j–k bond in an i–j–k–l torsion.
- Some force fields let *n* be positive or negative which corresponds to *d* = 1 or –1 for the harmonic style.

A style of *none* means dihedral forces are not computed, even if dhedrals are defined.

---

The *charmm* style uses the potential



$$E = K[1 + \cos(n\phi + d)]$$

K, d, and n are coefficients defined for each dihedral type. Additionally, a weighting factor is defined (see the dihedral coeff command) which is applied to the pairwise LJ and Coulombic interaction between the 1st and 4th atom in the dihedral quadruplet. Note that this weighting factor is unrelated to the weighting factor specified by the special bonds command which applies to all 1–4 interactions in the system. For CHARMM force fields, the latter should typically be set to 0.0, else the 1–4 interactions in a dihedral will be computed twice (once in the pair routine, and once by the charmm/dihedral routine).

---

The *class2* style uses the potential

$$\begin{aligned} E &= E_d + E_{mbt} + E_{ebt} + E_{at} + E_{aat} + E_{bb13} \\ E_d &= \sum_{n=1}^3 K_n [1 - \cos(n\phi - \phi_n)] \\ E_{mbt} &= (r_{jk} - r_2)[A_1 \cos(\phi) + A_2 \cos(2\phi) + A_3 \cos(3\phi)] \\ E_{ebt} &= (r_{ij} - r_1)[B_1 \cos(\phi) + B_2 \cos(2\phi) + B_3 \cos(3\phi)] + \\ &\quad (r_{kl} - r_3)[C_1 \cos(\phi) + C_2 \cos(2\phi) + C_3 \cos(3\phi)] \\ E_{at} &= (\theta_{ijk} - \theta_1)[D_1 \cos(\phi) + D_2 \cos(2\phi) + D_3 \cos(3\phi)] + \\ &\quad (\theta_{jkl} - \theta_2)[E_1 \cos(\phi) + E_2 \cos(2\phi) + E_3 \cos(3\phi)] \\ E_{aat} &= M(\theta_{ijk} - \theta_1)(\theta_{jkl} - \theta_2) \cos(\phi) \\ E_{bb13} &= N(r_{ij} - r_1)(r_{kl} - r_3) \end{aligned}$$

where  $E_d$  is the dihedral term,  $E_{mbt}$  is a middle–bond–torsion term,  $E_{ebt}$  is an end–bond–torsion term,  $E_{at}$  is an angle–torsion term,  $E_{aat}$  is an angle–angle–torsion term, and  $E_{bb13}$  is a bond–bond–13 term.

Theta1 and theta2 are equilibrium angles and  $r_1$   $r_2$   $r_3$  are equilibrium bond lengths.  $K_n$ ,  $A_n$ ,  $B_n$ ,  $C_n$ ,  $D_n$ ,  $E_n$ ,  $M$ ,  $N$ ,  $\Phi_n$ , theta1, theta2,  $r_1$ ,  $r_2$ ,  $r_3$  are coefficients defined for each dihedral type.

---

The *harmonic* style uses the potential

$$E = K[1 + d \cos(n\phi)]$$

K, d, and n are coefficients defined for each dihedral type.

---

The *helix* style uses the potential

$$E = A[1 - \cos(\theta)] + B[1 + \cos(3\theta)] + C[1 + \cos(\theta + \frac{\pi}{4})]$$

A, B, C are coefficients defined for each dihedral type.

This coarse–grain dihedral potential is described in (Guo). For dihedral angles in the helical region, the energy function is represented by a standard potential consisting of three minima, one corresponding to the

trans (t) state and the other to gauche states (g+ and g-). The paper describes how the A,B,C parameters are chosen so as to balance secondary (largely driven by local interactions) and tertiary structure (driven by long-range interactions).

---

The *multi/harmonic* style uses the potential

$$E = \sum_{n=1,5} A_n \cos^{n-1}(\phi)$$

A1, A2, A3, A4, and A5 are coefficients defined for each dihedral type.

---

The *opls* style uses the potential

$$E = \frac{1}{2}K_1[1 + \cos(\phi)] + \frac{1}{2}K_2[1 - \cos(2\phi)] + \frac{1}{2}K_3[1 + \cos(3\phi)] + \frac{1}{2}K_4[1 - \cos(4\phi)]$$

Note that the usual 1/2 factor is not included in the K values. K1, K2, K3, K4 are coefficients defined for each dihedral type.

This dihedral potential is used in the OPLS force field and is described in [\(Watkins\)](#).

---

The *hybrid* style enables the use of multiple dihedral styles in one simulation. A dihedral style is assigned to each dihedral type. For example, dihedrals in a polymer flow (of dihedral type 1) could be computed with a *charmm* potential and dihedrals in the wall boundary (of dihedral type 2) could be computed with a *harmonic* potential. The assignment of dihedral type to style is made via the [dihedral\\_coeff](#) command or in the data file.

---

### Restrictions:

Dihedral styles can only be set for atom styles that allow dihedrals to be defined.

Dihedral styles are part of the "molecular" package. They are only enabled if LAMMPS was built with that package. See the [Making LAMMPS](#) section for more info.

### Related commands:

[dihedral\\_coeff](#)

### Default:

dihedral\_style none

---

(**Guo**) Guo and Thirumalai, Journal of Molecular Biology, 263, 323–43 (1996).

(**Watkins**) Watkins and Jorgensen, J Phys Chem A, 105, 4118–4125 (2001).

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---

## dimension command

### Syntax:

```
dimension N
```

- $N = 2$  or  $3$

### Examples:

```
dimension 2
```

### Description:

Set the dimensionality of the simulation. By default LAMMPS runs 3d simulations. To run a 2d simulation, this command should be used prior to setting up a simulation box via the [create\\_box](#) or [read\\_data](#) commands. Restart files also store this setting.

See the discussion in [this section](#) for additional instructions on how to run 2d simulations.

### Restrictions:

This command must be used before the simulation box is defined by a [read\\_data](#) or [create\\_box](#) command.

### Related commands:

[fix enforce2d](#)

### Default:

```
dimension 3
```

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---

## dipole command

### Syntax:

```
dipole I value
```

- $I$  = atom type (see asterik form below)
- value = dipole

### Examples:

```
dipole 1 1.0  
dipole 3 2.0  
dipole 3*5 0.0
```

### Description:

Set the dipole moment for all atoms of one or more atom types. This command is only used for atom styles that require dipole moments ([atom style](#) dipole). A value of 0.0 should be used if the atom type has no dipole moment. Dipole values can also be set in the [read\\_data](#) data file. See the [units](#) command for a discussion of dipole units.

It can be specified in one of two ways. An explicit numeric value can be used, as in the 1st example above. Or a wild-card asterik can be used to set the dipole moment for multiple atom types. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If N = the number of atom types, then an asterik with no numeric values means all types from 1 to N. A leading asterik means all types from 1 to n (inclusive). A trailing asterik means all types from n to N (inclusive). A middle asterik means all types from m to n (inclusive).

A line in a data file that specifies a dipole moment uses the exact same format as the arguments of the dipole command in an input script, except that no wild-card asterik can be used. For example, under the "Dipoles" section of a data file, the line that corresponds to the 1st example above would be listed as

```
1 1.0
```

### Restrictions:

This command must come after the simulation box is defined by a [read\\_data](#), [read\\_restart](#), or [create\\_box](#) command.

All dipoles moments must be defined before a simulation is run (if the atom style requires dipoles be set).

**Related commands:** none

**Default:** none

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---

## displace\_atoms command

### Syntax:

```
displace_atoms group-ID style args keyword value ...
```

- group-ID = ID of group of atoms to displace
- style = *move* or *ramp*

```
move args = delx dely delz
    delx,dely,delz = distance to displace in each dimension (distance units)
ramp args = ddim dlo dhi dim clo chi
    ddim = x or y or z
    dlo,dhi = displacement distance between dlo and dhi (distance units)
    dim = x or y or z
    clo,chi = lower and upper bound of domain to displace (distance units)
```

- zero or more keyword/value pairs may be appended to the args

```
keyword = units
value = box or lattice
```

### Examples:

displace\_atoms command

```
displace_atoms top move 0 -5 0 units box
displace_atoms flow ramp x 0.0 5.0 y 2.0 20.5
```

### Description:

Displace a group of atoms. This can be useful to move atoms a large distance before beginning a simulation. For example, in a shear simulation, an initial strain can be imposed on the system. Or two groups of atoms can be brought into closer proximity.

The *move* style displaces the group of atoms by the specified 3d distance. The *ramp* style displaces atoms a variable amount in one dimension depending on the atom's coordinate in a (possibly) different dimension. For example, the second example command displaces atoms in the x-direction an amount between 0.0 and 5.0 distance units. Each atom's displacement depends on the fractional distance its y coordinate is between 2.0 and 20.5. Atoms with y-coordinates outside those bounds will be moved the minimum (0.0) or maximum (5.0) amount.

Distance units for the displacement are determined by the setting of *box* or *lattice* for the *units* keyword. *Box* means distance units as defined by the units command – e.g. Angstroms for *real* units. *Lattice* means to use lattice spacings as defined by the lattice command. The default is to use lattice units.

Care should be taken not to move atoms on top of other atoms. After the move, atoms are remapped to the periodic simulation box. In parallel, atoms should not be moved so far that they cross more than one processor's sub-domain, else they may be lost. If this is a problem, successive `displace_atom` commands can be used to move a greater distance.

### Restrictions:

This command requires inter-processor communication to migrate atoms once they have been displaced. This means that your system must be ready to perform a simulation before using this command (force fields setup, atom masses set, etc).

**Related commands:** none

### Default:

The option defaults are `units = lattice`.

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---

## dump command

### Syntax:

```
dump ID group-ID style N file args
```

- ID = user-assigned name for the dump
- group-ID = ID of the group of atoms to be dumped
- style = *atom* or *bond* or *custom* or *dcd* or *xtc* or *xyz*
- N = dump every this many timesteps
- file = name of file to write dump info to
- args = list of arguments for a particular style

```

atom args = none
bond args = none
custom args = list of atom attributes
    possible attributes = tag, mol, type, x, y, z, xs, ys, zs, xu, yu, zu,
                        ix, iy, iz, vx, vy, vz, fx, fy, fz,
                        q, mux, muy, muz, tqx, tqy, tqz,
                        centro, eng, sxx, syy, szz, sxy, sxz, syz
    tag = atom ID
    mol = molecule ID
    type = atom type
    x,y,z = unscaled atom coordinates
    xs,ys,zs = scaled atom coordinates
    xu,yu,zu = unwrapped atom coordinates
    ix,iy,iz = box image that the atom is in in
    vx,vy,vz = atom velocities
    fx,fy,fz = forces on atoms
    q = atom charge
    mux,muy,muz = orientation of dipolar atom
    tqx,tqy,tqz = torque on dipolar atoms
    centro = per-atom centro-symmetry parameter
    eng = per-atom pairwise energy
    sxx, syy, szz, sxy, sxz, syz = per-atom stress tensor components
dcd args = none
xtc args = precision (optional)
    precision = power-of-10 value from 10 to 1000000 (default = 1000)
xyz args = none

```

## Examples:

```

dump myDump all atom 100 dump.atom
dump 2 subgroup atom 50 dump.run.bin
dump 4a all custom 100 dump.myforce.* tag type x y vx fx
dump 4b flow custom 100 dump.%.myforce tag type eng sxx syy szz
dump 1 all xtc 1000 file.xtc 100.0

```

## Description:

Dump a snapshot of atom quantities to one or more files every so many timesteps in one of several styles. As described below, the filename determines the kind of output (text or binary or gzipped, one big file or one per timestep, one big file or one per processor). Only information for atoms in the specified group is dumped. The dump\_modify command can also alter what atoms are included. Not all styles support all these options; see details below.

Note that because periodic boundary conditions are enforced only on timesteps when neighbor lists are rebuilt, the coordinates of an atom written to a dump file may be slightly outside the simulation box.

Also note that when LAMMPS is running in parallel, the atom information written to dump files (typically one line per atom) may be written in an indeterminate order. This is because data for a single snapshot is collected from multiple processors. This is always the case for the *atom*, *bond*, and *custom* styles. It is also the case for the *xyz* style if the dump group is not *all*. It is not the case for the *dcd* and *xtc* styles which always write atoms in sorted order. So does the *xyz* style if the dump group is *all*.

---

The *style* keyword determines what atom quantities are written to the file and in what format. Settings made via the dump\_modify command can also alter the format of individual values and the file itself.

The *atom*, *bond*, and *custom* styles create files in a simple text format that is self-explanatory. Many of the

LAMMPS post-processing tools, including Pizza.py, work with this format.

For style *atom*, atom coordinates are written to the file, along with the atom ID and atom type. By default, atom coords are written in a scaled format (from 0 to 1). I.e. an x value of 0.25 means the atom is at a location 1/4 of the distance from xlo to xhi of the box boundaries. The format can be changed to unscaled coords via the dump\_modify settings. Image flags can also be added for each atom via dump\_modify.

For style *bond*, the bond topology between atoms is written, in the same format specified in data files read in by the read\_data command. Both atoms in the bond must be in the dump group for the bond to be written. Any bonds that have been broken (see the bond\_style command) by setting their bond type to 0 are not written. Bonds that have been turned off (see the fix\_shake or delete\_bonds commands) by setting their bond type negative are written into the file.

Style *custom* allows you to specify a list of atom attributes to be written to the dump file for each atom. Possible attributes are listed above and will appear in the order specified. Be careful not to specify a quantity that is not defined for a particular simulation – such as *q* for atom style *bond*, since that atom style doesn't assign charges. Dumps occur at the very end of a timestep, so atom attributes will include effects due to fixes that are applied during the timestep. An explanation of some of the dump custom quantities is given below.

The *dcd* style writes DCD files, a standard atomic trajectory format used by the CHARMM, NAMD, and XPlor molecular dynamics packages. DCD files are binary and thus may not be portable to different machines. The dump group must be *all* for the *dcd* style.

The *xtc* style writes XTC files, a compressed trajectory format used by the Gromacs molecular dynamics package, and described here. The precision used in XTC files can be specified; for example, a value of 100 means that coordinates are stored to 1/100 nanometer accuracy. XTC files are portable binary files written in the NFS XDR data format, so that any machine which supports XDR should be able to read them. The dump group must be *all* for the *xtc* style.

The *xyz* style writes XYZ files, which is a simple text-based coordinate format that many codes can read.

Note that DCD, XTC, and XYZ formatted files can be read directly by VMD (a popular molecular viewing program). VMD will also read LAMMPS *atom* style dump files since someone added a LAMMPS plug-in to VMD. I am told it requires an initial snapshot from an XYZ formatted file to get started.

---

Dumps are performed on timesteps that are a multiple of N and on the first and last timestep of a simulation, excluding duplicate timesteps. N must be > 0. N can be changed between runs by using the dump\_modify command (not allowed for *dcd* style).

The specified filename determines how the dump file(s) is written. The default is to write one large text file, which is opened when the dump command is invoked and closed when an undump command is used or when LAMMPS exits. For the *dcd* and *xtc* styles, this is a single large binary file.

If a '\*' character appears in the filename, then one file per snapshot is written and the '\*' character is replaced with the timestep value. For example, tmp.dump.\* becomes tmp.dump.0, tmp.dump.10000, tmp.dump.20000, etc. This option is not available for the *dcd* and *xtc* styles.

If a '%' character appears in the filename, then one file is written for each processor and the '%' character is replaced with the processor ID from 0 to P-1. For example, tmp.dump.% becomes tmp.dump.0, tmp.dump.1, ... tmp.dump.P-1, etc. This can be a fast mode of output on parallel machines that support parallel I/O. This option is not available for the *dcd*, *xtc*, and *xyz* styles.

Note that the '\*' and '%' characters can be used together to produce a large number of small dump files!

If the filename ends with ".bin", the dump file (or files, if '\*' or '%' is also used) is written in binary format. A binary dump file will be about the same size as a text version, but will typically write out much faster. Of course, when post-processing, you will need to convert it back to text format (see the [binary2txt tool](#)) or write your own code to read the binary file. The format of the binary file can be understood by looking at the `tools/binary2txt.cpp` file. This option is only available for the *atom* and *custom* styles.

If the filename ends with ".gz", the dump file (or files, if '\*' or '%' is also used) is written in gzipped format. A gzipped dump file will be about 3x smaller than the text version, but will also take longer to write. This option is not available for the *dcd* and *xtc* styles.

---

This section explains the atom quantities that can be specified as part of the *custom* style.

The *tag*, *mol*, *type*, *x*, *y*, *z*, *vx*, *vy*, *vz*, *fx*, *fy*, *fz*, *q* attributes are self-explanatory. *Tag* is the atom ID. *Mol* is the molecule ID, included in the data file for molecular systems. The *x*, *y*, *z* attributes write atom coordinates "unscaled", in the appropriate distance units (Angstroms, sigma, etc). Use *xs*, *ys*, *zs* if you want the coordinates "scaled" to the box size, so that each value is 0.0 to 1.0. Use *xu*, *yu*, *zu* if you want the coordinates "unwrapped" by the image flags for each atom. Unwrapped means that if the atom has passed thru a periodic boundary one or more times, the value is printed for what the coordinate would be if it had not been wrapped back into the periodic box. Note that using *xu*, *yu*, *zu* means that the coordinate values may be far outside the box size printed with the snapshot. The image flags can be printed directly using the *ix*, *iy*, *iz* attributes. The [dump\\_modify](#) documentation describes in more detail what is meant by scaled vs unscaled coordinates and the image flags.

The *mux*, *muy*, *muz*, *tqy*, *tqx*, *tqz* attributes are specific to dipolar systems defined with an atom style of *dipole*.

The *centro* attribute causes the centro-symmetry parameter to be computed for each atom in the dump group using the following formula from [\(Kelchner\)](#)

$$P = \sum_{i=1}^6 |\vec{R}_i + \vec{R}_{i+6}|^2$$

where the 12 nearest neighbors are found and  $\vec{R}_i$  and  $\vec{R}_{i+6}$  are the vectors from the central atom to the opposite pair of nearest neighbors. In solid state systems this is a useful measure of the local lattice disorder around an atom and can be used to characterize whether the atom is part of a perfect lattice, a local defect (e.g. a dislocation or stacking fault), or at a surface. The neighbor list needed to compute this quantity is constructed each time the dump is performed. Thus it can be inefficient to dump this quantity too frequently or to have multiple dump commands, each with a *centro* attribute.

The *eng* attribute computes the pairwise energy for each atom. This is its pairwise interaction with all of its neighbors (divided by 2). Summed over all atoms, this should equal the pairwise energy of the entire system (Van der Waals + Coulombic). However, for force fields that include a contribution to the pairwise energy that is computed as part of dihedral terms (i.e. 1-4 interactions), this contribution is not included in the per-atom pairwise energy. Computation of the per-atom energy requires a loop thru the neighbor list and inter-processor communication, so it can be inefficient to dump this quantity too frequently or to have multiple dump commands, each with a *eng* attribute.

The *sxx*, *syy*, *szz*, *sxy*, *sxz*, *syx* attributes compute the pairwise stress tensor for each atom where the *ab*



component of the stress on atom  $i$  is given by

$$S_{ab} = - \left[ m v_a v_b + \frac{1}{2} \sum_{j=1}^N (a_i - a_j) F_{bij} \right]$$

where the first term is a kinetic energy component for atom  $i$ ,  $j$  loops over the  $N$  neighbors of atom  $i$ , and  $Fb$  is one of 3 components of force on atom  $i$  due to atom  $j$ . Both  $a$  and  $b$  can take on values x,y,z to generate the 6 components of the symmetric tensor.

Note that this formula for stress does not include virial contributions from intra-molecular interactions (e.g. bonds, angles, torsions, etc). Also note that this quantity is the negative of the per-atom pressure tensor. It is also really a stress-volume formulation. It would need to be divided by a per-atom volume to have units of stress, but an individual atom's volume is not easy to compute in a deformed solid. Computation of stress tensor components requires a loop thru the neighbor list and inter-processor communication, so it can be inefficient to dump this quantity too frequently or to have multiple dump commands, each with stress tensor attributes.

See [this section](#) for information on how to modify LAMMPS to dump other kinds of per-atom quantities.

---

#### Restrictions:

To write gzipped dump files, you must compile LAMMPS with the `-DGZIP` option – see the [Making LAMMPS](#) section of the documentation.

The *bond* style is part of the "molecular" package. It is only enabled if LAMMPS was built with that package. See the [Making LAMMPS](#) section for more info.

The *xtc* style is part of the "xtc" package. It is only enabled if LAMMPS was built with that package. See the [Making LAMMPS](#) section for more info. This is because some machines may not support the lo-level XDR data format that XTC files are written with, which will result in a compile-time error when a lo-level include file is not found. Putting this style in a package makes it easy to exclude from a LAMMPS build for those machines.

Granular systems and granular pair potentials cannot be used to compute per-atom energy and stress. The [fix gran/diag](#) command should be used instead.

#### Related commands:

[dump\\_modify](#), [undump](#)

**Default:** none

---

(**Kelchner**) Kelchner, Plimpton, Hamilton, Phys Rev B, 58, 11085 (1998).

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## dump\_modify command

### Syntax:

dump\_modify dump-ID keyword args ...

- dump-ID = ID of dump to modify
- one or more keyword/arg pairs may be appended
- keyword = *format* or *scale* or *image* or *header* or *flush* or *region* or *thresh*

*format* arg = C-style format string for one line of output  
*scale* arg = *yes* or *no*  
*image* arg = *yes* or *no*  
*flush* arg = *yes* or *no*  
*every* arg = N  
N = dump every this many timesteps  
*region* arg = region-ID or "none"  
*thresh* args = attribute operation value  
attribute = same attributes (x,fy,eng,sxx,etc) used by dump custom style  
operation = <or <= or > or >= or = or  
value = numeric value to compare to  
these 3 args can be replaced by the word "none" to turn off thresholding

### Examples:

```
dump_modify 1 format "%d %d %20.15g %g %g" scale yes
dump_modify myDump image yes scale no flush yes
dump_modify 1 region mySphere thresh x <0.0 thresh energy >= 3.2
```

### Description:

Modify the parameters of a previously defined dump command. Not all parameters are relevant to all dump styles.

The text-based dump styles have a default C-style format string which simply specifies %d for integers and %g for real values. The *format* keyword can be used to override the default with a new C-style format string. Do not include a trailing "\n" newline character in the format string. This option has no effect on the *dcd* and *xtc* dump styles since they write binary files.

The *scale* and *image* keywords apply only to the dump *atom* style. A scale value of *yes* means atom coords are written in normalized units from 0.0 to 1.0 in each box dimension. A value of *no* means they are written in absolute distance units (e.g. Angstroms or sigma). If the image value is *yes*, 3 flags are appended to each atom's coords which are the absolute box image of the atom in each dimension. For example, an x image flag of -2 with a normalized coord of 0.5 means the atom is in the center of the box, but has passed thru the box boundary 2 times and is really 2 box lengths to the left of its current coordinate. Note that for dump style *custom* these values can be printed in the dump file by using the appropriate atom attributes in the dump command itself.

The *flush* option determines whether a flush operation is invoked after a dump snapshot is written to the dump file. A flush insures the output in that file is current (no buffering by the OS), even if LAMMPS halts before the simulation completes. Flushes cannot be performed with dump style *xtc*.

The *every* option changes the dump frequency originally specified by the [dump](#) command to a new value which must be > 0. The dump frequency cannot be changed for the dump *dcd* style.

The *region* keyword only applies to the dump *custom* style. If specified, only atoms in the region will be written to the dump file. Only one region can be applied as a filter (the last one specified). See the [region](#) command for more details. Note that a region can be defined as the "inside" or "outside" of a geometric shape, and it can be the "union" or "intersection" of a series of simpler regions.

The *thresh* keyword only applies to the dump *custom* style. Multiple thresholds can be specified. Specifying "none" turns off all threshold criteria. If thresholds are specified, only atoms whose attributes meet all the threshold criteria are written to the dump file. The possible attributes that can be tested for are the same as those that can be specified in the [dump custom](#) command. Note that different attributes can be output by the dump custom command than are used as threshold criteria by the dump\_modify command. E.g. you can output the coordinates and stress of atoms whose energy is above some threshold.

**Restrictions:** none

**Related commands:**

[dump](#), [undump](#)

**Default:**

The option defaults are format = %d and %g for each integer or floating point value, scale = yes, image = no, flush = yes (except for dump *xtc* style), region = none, and thresh = none.

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## echo command

**Syntax:**

```
echo style
```

- style = *none* or *screen* or *log* or *both*

**Examples:**

```
echo both
echo log
```

**Description:**

This command determines whether LAMMPS echoes each input script command to the screen and/or log file as it is read and processed. If an input script has errors, it can be useful to look at echoed output to see the last command processed.

**Restrictions:** none

**Related commands:** none

## Default:

echo log

## fix command

### Syntax:

```
fix ID group-ID style args
```

- ID = user-assigned name for the fix
- group-ID = ID of the group of atoms to apply the fix to
- style = one of a long list of possible style names (see below)
- args = arguments used by a particular style

### Examples:

```
fix 1 all nve  
fix 3 all nvt 300.0 300.0 0.01  
fix mine top setforce 0.0 NULL 0.0
```

### Description:

Set a fix that will be applied to a group of atoms. In LAMMPS, a "fix" is any operation that is applied to the system during timestepping or minimization. Examples include updating of atom positions and velocities due to time integration, controlling temperature, applying constraint forces to atoms, enforcing boundary conditions, computing diagnostics, etc. There are dozens of fixes defined in LAMMPS and new ones can be added – see [this section](#) for a discussion.

Each fix style has its own documentation page which describes its arguments and what it does. For example, see the [fix setforce](#) page for information on style *setforce*.

Fixes perform their operations at different stages of the timestep. If 2 or more fixes both operate at the same stage of the timestep, they are invoked in the order they were specified in the input script.

Specifying a new fix with the same ID as an existing fix effectively replaces the old fix (and its parameters) with the new fix. This can only be done if the new fix has the same style as the existing fix.

Fixes can be deleted with the [unfix](#) command. Note that this is the only way to turn off a fix; simply specifying a new fix with a similar style will not turn off the first one. For example, using a "fix nve" command for a second run after using a "fix nvt" command for the first run, will not cancel out the NVT time integration invoked by the "fix nvt" command. Thus two time integrators would be in place!

Here is an alphabetic list of fix styles defined in LAMMPS:

- [fix addforce](#) – add a force to each atom
- [fix aveforce](#) – add an averaged force to each atom
- [fix com](#) – compute a center-of-mass
- [fix drag](#) – drag atoms towards a defined coordinate

- fix efield – impose electric field on system
- fix enforce2d – zero out z–dimension velocity and force
- fix freeze – freeze atoms in a granular simulation
- fix gran/diag – compute granular diagnostics
- fix gravity – add gravity to atoms in a granular simulation
- fix indent – impose force due to an indenter
- fix insert – add new atoms to a granular simulation
- fix langevin – Langevin temperature control
- fix lineforce – constrain atoms to move in a line
- fix msd – compute mean–squared displacement (i.e. diffusion coefficient)
- fix nph – constant NPH time integration via Nose/Hoover
- fix npt – constant NPT time integration via Nose/Hoover
- fix nve – constant NVE time integration
- fix nve/gran – NVE time integration for granular systems
- fix nvt – constant NVT time integration via Nose/Hoover
- fix orient/fcc – add grain boundary migration force
- fix planeforce – constrain atoms to move in a plane
- fix poems – constrain clusters of atoms to move as coupled rigid bodies
- fix print – print text and variables during a simulation
- fix rdf – compute radial distribution functions
- fix rigid – constrain one or more clusters of atoms to move as a rigid body
- fix setforce – set the force on each atom
- fix shake – SHAKE constraints on bonds and/or angles
- fix spring – apply harmonic spring force to group of atoms
- fix spring/rg – spring on radius of gyration of group of atoms
- fix spring/self – spring from each atom to its origin
- fix temp/rescale – temperature control by velocity rescaling
- fix tmd – guide a group of atoms to a new configuration
- fix uniaxial – uniaxial straining of system while preserving total volume
- fix viscous – viscous damping for granular simulations
- fix volume/rescale – density control by volume rescaling
- fix wall/gran – frictional wall(s) for granular simulations
- fix wall/lj93 – Lennard–Jones 9/3 wall
- fix wall/reflect – reflecting wall(s)
- fix wiggle – oscillate walls and frozen atoms

### Restrictions:

Some fix styles are part of specific packages. They are only enabled if LAMMPS was built with that package. See the Making LAMMPS section for more info.

The *freeze*, *gran/diag*, *gravity*, *insert*, *nve/gran*, and *wall/gran* styles are part of the "granular" package.

The *poems* style is part of the "poems" package.

### Related commands:

unfix, fix modify

**Default:** none

## fix addforce command

### Syntax:

```
fix ID group-ID addforce fx fy fz
```

- ID, group-ID are documented in [fix](#) command
- addforce = style name of this fix command
- fx,fy,fz = force component values (force units)

### Examples:

```
fix kick flow addforce 1.0 0.0 0.0
```

### Description:

Add fx,fy,fz to the corresponding component of force for each atom in the group. This command can be used to give an additional push to atoms in a simulation, such as for a simulation of Poiseuille flow in a channel.

**Restrictions:** none

### Related commands:

[fix setforce](#), [fix aveforce](#)

**Default:** none

## fix aveforce command

### Syntax:

```
fix ID group-ID aveforce fx fy fz
```

- ID, group-ID are documented in [fix](#) command
- aveforce = style name of this fix command
- fx,fy,fz = force component values (force units)

### Examples:

```
fix pressdown topwall aveforce 0.0 -1.0 0.0  
fix 2 bottomwall aveforce NULL -1.0 0.0
```

### Description:

Apply an additional external force to a group of atoms in such a way that every atom experiences the same force. This is useful for pushing on wall or boundary atoms so that the structure of the wall does not change over time.

The existing force is averaged for the group of atoms, component by component. The actual force on each atom is then set to the average value plus the component specified in this command. This means each atom in the group receives the same force.

If any of the arguments is specified as NULL then the forces in that dimension are not changed. Note that this is not the same as specifying a 0.0 value, since that sets all forces to the same average value without adding in any additional force.

**Restrictions:** none

**Related commands:**

[fix setforce](#), [fix addforce](#)

**Default:** none

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---

## fix com command

**Syntax:**

```
fix ID group-ID com N file
```

- ID, group-ID are documented in [fix](#) command
- com = style name of this fix command
- N = compute center-of-mass every this many timesteps
- file = filename to write center-of-mass info to

**Examples:**

```
fix 1 all com 100 com.out
```

**Description:**

Compute the center-of-mass of the group of atoms every N steps, including all effects due to atoms passing thru periodic boundaries. Write the results to the specified file.

**Restrictions:** none

**Related commands:** none

**Default:** none

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## fix drag command

### Syntax:

```
fix ID group-ID drag x y z fmag delta
```

- ID, group-ID are documented in [fix](#) command
- drag = style name of this fix command
- x,y,z = coord to drag atoms towards
- fmag = magnitude of force to apply to each atom (force units)
- delta = cutoff distance inside of which force is not applied (distance units)

### Examples:

```
fix center small-molecule drag 0.0 10.0 0.0 5.0 2.0
```

### Description:

Apply a force to each atom in a group to drag it towards the point (x,y,z). The magnitude of the force is specified by fmag. If an atom is closer than a distance delta to the point, then the force is not applied.

Any of the x,y,z values can be specified as NULL which means do not include that dimension in the distance calculation or force application.

This command can be used to steer one or more atoms to a new location in the simulation.

**Restrictions:** none

**Related commands:**

[fix spring](#)

**Default:** none

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---

## fix efield command

### Syntax:

```
fix ID group-ID efield ex ey ez
```

- ID, group-ID are documented in [fix](#) command
- efield = style name of this fix command
- ex,ey,ez = E-field component values (electric field units)

### Examples:

```
fix kick external-field efield 1.0 0.0 0.0
```

### Description:

fix drag command



Add a force  $F = qE$  to each charged atom in the group due to an external electric field being applied to the system.

**Restrictions:** none

**Related commands:**

[fix addforce](#)

**Default:** none

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---

## fix enforce2d command

**Syntax:**

```
fix ID group-ID enforce2d
```

- ID, group-ID are documented in [fix](#) command
- enforce2d = style name of this fix command

**Examples:**

```
fix 5 all enforce2d
```

**Description:**

Zero out the z-dimension velocity and force on each atom in the group. This is useful when running a 2d simulation to insure that atoms do not move from their initial z coordinate.

**Restrictions:** none

**Related commands:** none

**Default:** none

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## fix freeze command

**Syntax:**

```
fix ID group-ID freeze
```

- ID, group-ID are documented in [fix](#) command
- freeze = style name of this fix command

**Examples:**

```
fix 2 bottom freeze
```

fix enforce2d command

**Description:**

Zero out the force and torque on a granular particle. This is useful for preventing certain particles from moving in a simulation.

**Restrictions:**

Can only be used if LAMMPS was built with the "granular" package. Can only be used with atom\_style granular.

There can only be a single freeze fix defined. This is because other parts of the code (pair potentials, thermodynamics, etc) treat frozen particles differently and need to be able to reference a single group to which this fix is applied.

**Related commands:** none

[atom\\_style granular](#)

**Default:** none

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---

## fix gran/diag command

**Syntax:**

```
fix ID group-ID gran/diag nevery file zlayer
```

- ID, group-ID are documented in [fix](#) command
- gran/diag = style name of this fix command
- nevery = compute diagnostics every this many timesteps
- file = filename to store diagnostic info in
- zlayer = bin size in z dimension

**Examples:**

```
fix 1 all gran/diag 1000 tmp 0.9
```

**Description:**

Compute aggregate density, velocity, and stress diagnostics for a group of granular atoms as a function of z depth in the granular system. The results are written to 3 files named file.den, file.vel, and file.str. The z bins begin at the bottom of the system and extend upward with a thickness of zlayer for each bin. The quantities written to the file are averaged over all atoms in the bin.

**Restrictions:**

Can only be used if LAMMPS was built with the "granular" package. Can only be used with atom\_style granular.

**Related commands:**

fix gran/diag command

**Default:** none

## fix gravity command

### Syntax:

```
fix ID group gravity style args
```

- ID, group are documented in fix command
- gravity = style name of this fix command
- style = *chute* or *spherical* or *gradient* or *vector*

```
chute args = angle
  angle = angle in +x away from -z axis (in degrees)
spherical args = phi theta
  phi = azimuthal angle from +x axis (in degrees)
  theta = angle from +z axis (in degrees)
gradient args = phi theta phi_grad theta_grad
  phi = azimuthal angle from +x axis (in degrees)
  theta = angle from +z axis (in degrees)
  phi_grad = rate of change of angle phi (full rotations per time unit)
  theta_grad = rate of change of angle theta
              (full rotations per time unit)
vector args = magnitude x y z
  magnitude = size of acceleration (force/mass units)
  x y z = vector direction to apply the acceleration
```

### Examples:

```
fix 1 all gravity chute 24.0
fix 1 all gravity spherical 0.0 -180.0
fix 1 all gravity gradient 0.0 -180.0 0.0 0.1
fix 1 all gravity vector 100.0 1 1 0
```

### Description:

Impose an additional acceleration on each particle in the group. For granular systems the magnitude is chosen so as to be due to gravity. For non-granular systems the magnitude of the acceleration is specified, so it can be any kind of driving field desired (e.g. a pressure gradient inducing a Poisselle flow). Note that this is different from what the fix addforce command does, since it adds the same force to each atom, independent of its mass. This command adds the same acceleration to each atom (force/mass).

The first 3 styles apply to granular systems. Style *chute* is typically used for simulations of chute flow where the specified angle is the chute angle, with flow occurring in the +x direction. Style *spherical* allows an arbitrary 3d direction to be specified for the gravity vector. Style *gradient* allows the direction of the gravity vector to be time dependent. The units of the gradient arguments are in full rotations per time unit. E.g. a timestep of 0.001 and a gradient of 0.1 means the gravity vector would rotate thru 360 degrees every 10,000 timesteps. For the time-dependent case, the initial direction of the gravity vector is phi,theta at the time the fix is specified.

The strength of the acceleration due to gravity is 1.0 in LJ units, which are the only allowed units for granular systems.

Style *vector* is used for non-granular systems. An acceleration of the specified magnitude is applied to each atom in the group in the vector direction given by (x,y,z).

### Restrictions:

Styles *chute*, *spherical*, and *gradient* can only be used with atom\_style granular. Style *vector* can only be used with non-granular systems.

### Related commands:

atom\_style granular, fix addforce

**Default:** none

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## fix indent command

### Syntax:

```
fix ID group-ID indent k keyword args ...
```

- ID, group-ID are documented in fix command
- indent = style name of this fix command
- k = force constant for indenter surface (force/distance<sup>2</sup> units)
- one or more keyword/value pairs may be appended to the args
- keyword = *sphere* or *cylinder* or *vel* or *rstart* or *units*

```
sphere args = x y z R
  x,y,z = initial position of center of indenter
  R = sphere radius of indenter (distance units)
cylinder args = dim c1 c2 R
  dim = x or y or z = axis of cylinder
  c1,c2 = coords of cylinder axis in other 2 dimensions (distance units)
  R = cylinder radius of indenter (distance units)
vel args = vx vy vz
  vx,vy,vz = velocity of center of indenter (velocity units)
rstart value = R0
  R0 = sphere or cylinder radius at start of run
  R is value at end of run, so indenter expands/contracts over time
units value = lattice or box
  lattice = the geometry is defined in lattice units
  box = the geometry is defined in simulation box units
```

### Examples:

```
fix 1 all indent 10.0 sphere 0.0 0.0 15.0 3.0 vel 0.0 0.0 -1.0
fix 2 flow indent 10.0 cylinder z 0.0 0.0 10.0 units box
```

### Description:

Insert an indenter within a simulation box. The indenter repels all atoms that touch it, so it can be used to push into a material or as an obstacle in a flow.

The indenter can either be spherical or cylindrical. You must set one of those 2 keywords.

A spherical indenter exerts a force of magnitude

$$F(r) = -k (r - R)^2$$

on each atom where  $k$  is the specified force constant,  $r$  is the distance from the atom to the center of the indenter, and  $R$  is the radius of the indenter. The force is repulsive and  $F(r) = 0$  for  $r > R$ .

A cylindrical indenter exerts the same force, except that  $r$  is the distance from the atom to the center axis of the cylinder. The cylinder extends infinitely along its axis.

If the *vel* keyword is specified, the center (or axis) of the spherical (or cylindrical) indenter will move during the simulation, based on its initial position ( $x,y,z$ ) and the specified ( $v_x,v_y,v_z$ ). Note that if you do multiple runs, the initial position of the indenter ( $x,y,z$ ) does not change, so it will continue to move at the specified velocity.

If the *rstart* keyword is specified, then the radius of the indenter is a time-dependent quantity.  $R_0$  is the value assigned at the start of the run;  $R$  is the value at the end. At intermediate times, the radius is linearly interpolated between these two values. This option can be used, for example, to grow/shrink a void within the simulation box. This option is not relevant during an energy minimization; the indenter always has radius  $R$  in that case. Note that if you do multiple runs, you may need to re-specify the fix so that the indenter radius has the appropriate value. If you do nothing, it will be reset to  $R_0$  at the beginning of each run.

The *units* keyword determines the meaning of the distance units used to define the indenter. A *box* value selects standard distance units as defined by the units command, e.g. Angstroms for units = real or metal. A *lattice* value means the distance units are in cubic lattice spacings. The lattice command must first be used to define a lattice. Note that the units choice affects not only the indenter's physical geometry, but also its velocity and force constant since they are defined in terms of distance as well.

**Restrictions:** none

**Related commands:** none

**Default:**

The option defaults are *vel* = 0,0,0 and *units* = lattice.

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## fix insert command

**Syntax:**

```
fix ID group-ID insert N type seed keyword values ...
```

- ID, group-ID are documented in fix command
- insert = style name of this fix command

- N = # of atoms to insert
- type = atom type to assign to inserted atoms
- seed = random # seed
- one or more keyword/value pairs may be appended to args
- keyword = *region* or *diam* or *dens* or *vol* or *zrate* or *vel*

```

region value = region-ID
    region-ID = ID of region to use as insertion volume
diam values = lo hi
    lo,hi = range of diameters for inserted particles (distance units)
dens values = lo hi
    lo,hi = range of densities for inserted particles
vol values = fraction Nattempt
    fraction = desired volume fraction for filling insertion volume
    Nattempt = max # of insertion attempts per atom
zrate value = rate
    rate = z velocity at which insertion volume moves (velocity units)
vel values = vxlo vxhi vylo vyhi vz
    vxlo,vxhi = range of x velocities for inserted particles (velocity units)
    vylo,vyhi = range of y velocities for inserted particles (velocity units)
    vz = z velocity assigned to inserted particles (velocity units)

```

### Examples:

```

fix 3 all insert 1000 2 29494 region myblock
fix 2 all insert 10000 1 19985583 region disk vol 0.33 100 zrate 1.0 diam 0.9 1.1

```

### Description:

Insert particles into a granular run every few timesteps within a specified region until N particles have been inserted. This is useful for simulating the pouring of particles into a container.

Inserted particles are assigned the specified atom type and are assigned to two groups: the default group "all" and the group specified in the fix insert command (which can also be "all").

This command must use the *region* keyword to define an insertion volume. The specified region must have been previously defined with a *region* command. It must be of type *block* or a z-axis *cylinder* and must be defined with *side = in*.

Each timestep particles are inserted, they are placed randomly inside the insertion volume so as to mimic a stream of poured particles. The larger the volume, the more particles that can be inserted at any one timestep. Particles are inserted again after enough time has elapsed that the previously inserted particles fall out of the insertion volume under the influence of gravity. Insertions continue every so many timesteps until the desired # of particles has been inserted.

All other keywords are optional with defaults as shown below. The *diam*, *dens*, and *vel* options enable inserted particles to have a range of diameters or densities or xy velocities. The specific values for a particular inserted particle will be chosen randomly and uniformly between the specified bounds. The *vz* value for option *vel* assigns a z-velocity to each inserted particle.

The *vol* option specifies what volume fraction of the insertion volume will be filled with particles. The higher the value, the more particles are inserted each timestep. Since inserted particles cannot overlap, the maximum volume fraction should be no higher than about 0.6. LAMMPS will make up to Nattempt tries to insert a new particle without overlaps. If it fails it prints a warning.

The *zrate* option allows the insertion volume to move in the z direction. This enables pouring particles from a successively higher height over time.

### Restrictions:

Can only be used if LAMMPS was built with the "granular" package. Can only be used with *atom\_style granular*. A gravity fix in the -z direction must be defined for use in conjunction with this fix.

### Related commands:

[fix\\_gravity\\_region](#)

### Default:

The option defaults are *diam* = 1.0 1.0, *dens* = 1.0 1.0, *vol* = 0.25 50, *zrate* = 0.0, *vel* = 0.0 0.0 0.0 0.0 0.0.

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## fix langevin command

### Syntax:

```
fix ID group-ID langevin Tstart Tstop damp seed keyword values ...
```

- ID, group-ID are documented in [fix](#) command
- langevin = style name of this fix command
- Tstart,Tstop = desired temperature at start/end of run (temperature units)
- damp = damping parameter (time units)
- seed = random # seed to use for white noise (integer > 0 and < 900000000)
- zero or more keyword/value pairs may be appended to the args

```
keyword = axes or scale or region
axes values = xflag yflag zflag
xflag,yflag,zflag = 0/1 to exclude/include a dimension in the thermostat
scale values = type ratio
type = atom type (1-N)
ratio = factor to scale the damping coefficient by
region values = region-ID
region-ID = ID of region to apply thermostat to
```

### Examples:

```
fix 3 boundary langevin 1.0 1.0 1000.0 699483
fix 1 all langevin 1.0 1.1 100.0 48279 axes 0 1 1
fix 3 boundary langevin 1.0 1.0 1000.0 699483 region boundary
```

### Description:

Apply a Langevin thermostat to a group of atoms which models an interaction with a background implicit solvent. Used with [fix nve](#), this command performs Brownian dynamics (BD), since the total force on each atom will have the form:

$$\mathbf{F} = \mathbf{F}_c + \mathbf{F}_f + \mathbf{F}_r$$

Fc is the conservative force computed via the usual inter-particle interactions ([pair\\_style](#), [bond\\_style](#), etc).

The Ff and Fr terms are added by this fix. Ff =  $-\gamma v$  and is a frictional drag or viscous damping term proportional to the particle's velocity. Gamma for each atom is computed as  $m/\text{damp}$ , where m is the mass of the particle and damp is the damping factor specified by the user.

Fr is a force due to solvent atoms at a temperature T randomly bumping into the particle. As derived from the fluctuation/dissipation theorem, its magnitude is proportional to  $\sqrt{T m / \text{dt damp}}$ , where T is the desired temperature, m is the mass of the particle, dt is the timestep size, and damp is the damping factor. Random numbers are used to randomize the direction and magnitude of this force.

The desired temperature at each timestep is a ramped value during the run from *Tstart* to *Tstop*. The *damp* parameter is specified in time units and determines how rapidly the temperature is relaxed. For example, a value of 100.0 means to relax the temperature in a timespan of (roughly) 100 time units (tau or fmsec or psec – see the [units](#) command). The damp factor can be thought of as inversely related to the viscosity of the solvent. I.e. a small relaxation time implies a hi-viscosity solvent and vice versa. See the discussion about gamma and viscosity in the documentation for the [fix viscous](#) command for more details.

The random # *seed* should be a non-zero integer with 1 to 8 digits. A Marsaglia random number generator is used. Each processor uses the input seed to generate its own unique seed and its own stream of random numbers. Thus the dynamics of the system will not be identical on two runs on different numbers of processors. Also, the state of the random number generator is not saved in a restart file. This means you cannot do exact restarts when a fix *langevin* command is used.

The keyword *axes* can be used to specify which dimensions to add Ff and Fr to. A flag of 0 means skip that dimension; a flag of 1 means include that dimension. The default is 1 for all 3 dimensions.

The keyword *scale* allows the damp factor to be scaled up or down by the specified factor for atoms of that type. It can be used multiple times to adjust damp for several atom types. Note that specifying a ratio of 2 increase the relaxation time which is equivalent to the the solvent's viscosity acting on particles with 1/2 the diameter. This is the opposite effect of scale factors used by the [fix viscous](#) command, since the damp factor in fix *langevin* is inversely related to the gamma factor in fix *viscous*. Also note that the damping factor in fix *langevin* includes the particle mass in Ff, unlike fix *viscous*. Thus the mass and size of different atom types should be accounted for in the choice of ratio values.

The keyword *region* applies the fix only to atoms that are in the specified geometric region (and in the fix group). Since atoms can enter/leave a region, this test is performed each timestep.

As noted above, fix *langevin* does not update the coordinates or velocities of its atoms, only the forces. It is normally used with a [fix nve](#) that does the time integration. Fix *langevin* should not normally be used on atoms that also have their temperature controlled by another fix – e.g. a [nvt](#) or [temp/rescale](#) fix.

**Restrictions:** none

**Related commands:**

[fix nvt](#), [fix temp/rescale](#), [fix viscous](#)

**Default:** none

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## fix lineforce command

### Syntax:

```
fix ID group-ID lineforce x y z
```

- ID, group-ID are documented in [fix](#) command
- lineforce = style name of this fix command
- x y z = direction of line as a 3-vector

### Examples:

```
fix hold boundary lineforce 0.0 1.0 1.0
```

### Description:

Adjust the forces on each atom in the group so that it's motion will be along the linear direction specified by the vector (x,y,z). This is done by subtracting out components of force perpendicular to the line.

If the initial velocity of the atom is 0.0 (or along the line), then it should continue to move along the line thereafter.

**Restrictions:** none

**Related commands:**

[fix planeforce](#)

**Default:** none

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## fix\_modify command

### Syntax:

```
fix_modify fix-ID keyword value ...
```

- fix-ID = ID of the fix to modify
- one or more keyword/value pairs may be appended
- keyword = *temp* or *thermo* or *energy*

```
temp value = temperature ID
thermo value = yes or no
energy value = yes or no
```

### Examples:

```
fix_modify 3 temp myTemp
fix_modify 1 thermo yes energy no
```

**Description:**

Modify one or more parameters of a previously defined fix. Not all fix styles support all parameters.

The *temp* keyword is used to determine how a fix computes temperature. The specified temperature ID must have been previously defined by the user via the [temperature](#) command. The default setting for *temp* is temperature ID = *default*. Fix styles that use the *temp* setting are [temp/rescale](#), [nvt](#), and [npt](#).

The *thermo* and *energy* keywords enable a fix to compute and print quantities as part of the thermodynamic output to the screen and log file every so many timesteps (if they are defined as part of the fix). See the [thermo\\_style](#) command for how this printing is formatted. When the *thermo* keyword is set to yes, the fix prints one or more values. When the *energy* keyword is set to yes, the fix computes a contribution to the PotEng quantity (total potential energy) printed during thermodynamic output. The fixes that use this option include: [fix nvt](#), [fix npt](#), [fix nph](#), [fix temp/rescale](#), and [fix wall/lj93](#). See the individual fix commands for more info on what is printed.

**Restrictions:** none

**Related commands:**

[fix](#), [temperature](#), [thermo\\_style](#)

**Default:**

The option defaults are temp = default, thermo = no, energy = no.

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## fix msd command

**Syntax:**

```
fix ID group-ID msd N file
```

- ID, group-ID are documented in [fix](#) command
- msd = style name of this fix command
- N = compute mean-squared displacement every this many timesteps
- file = filename to write mean-squared displacement info to

**Examples:**

```
fix 1 all msd 100 diff.out
```

**Description:**

Compute the mean-squared displacement of the group of atoms every N steps, including all effects due to atoms passing thru periodic boundaries. The slope of the mean-squared displacement versus time is proportional to the diffusion coefficient of the diffusing atoms. The "origin" of the displacement for each atom is its position at the time the fix command was issued. Write the results to the specified file.

**Restrictions:** none

fix msd command

**Related commands:** none

**Default:** none

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## fix nph command

### Syntax:

```
fix ID group-ID nph p-style args keyword value ...
```

- ID, group-ID are documented in [fix](#) command
- nph = style name of this fix command
- p-style = *xyz* or *xy* or *yz* or *xz* or *aniso*

```
xyz args = Pstart Pstop Pdamp
  Pstart,Pstop = desired pressure at start/end of run (pressure units)
  Pdamp = pressure damping parameter (time units)
xy or yz or xz args = Px0 Px1 Py0 Py1 Pz0 Pz1 Pdamp
  Px0,Px1,Py0,Py1,Pz0,Pz1 = desired pressure in x,y,z at
  start/end (0/1) of run (pressure units)
  Pdamp = pressure damping parameter (time units)
aniso args = Px0 Px1 Py0 Py1 Pz0 Pz1 Pdamp
  Px0,Px1,Py0,Py1,Pz0,Pz1 = desired pressure in x,y,z at
  start/end (0/1) of run (pressure units)
  Pdamp = pressure damping parameter (time units)
```

- zero or more keyword/value pairs may be appended to the args
- keyword = *drag* or *dilate*

```
drag value = drag factor added to barostat (0.0 = no drag)
dilate value = all or partial
```

### Examples:

```
fix 1 all nph xyz 0.0 0.0 1000.0
fix 2 all nph xz 5.0 5.0 NULL NULL 5.0 5.0 1000.0 drag 1.0
fix 2 all nph aniso 0.0 0.0 0.0 0.0 NULL NULL 1000.0
```

### Description:

Perform constant NPH integration to update positions and velocities each timestep for atoms in the group using a Nose/Hoover pressure barostat. P is pressure. This creates a system trajectory consistent with the isobaric ensemble. Unlike [fix npt](#), temperature will not be controlled if no other fix is used. Temperature can be controlled independently by using "[fix langevin](#) or [fix temp/rescale](#).

The atoms in the fix group are the only ones whose velocities and positions are updated by the velocity/position update portion of the NPT integration.

Regardless of what atoms are in the fix group, a global pressure is computed for all atoms. Similarly, when the size of the simulation box is changed, all atoms are re-scaled to new positions, unless the keyword *dilate* is specified with a value of *partial*, in which case only the atoms in the fix group are re-scaled. The latter can be useful for leaving the coordinates of atoms in a solid substrate unchanged and controlling the pressure of a

surrounding fluid.

This fix computes a temperature each timestep, to contribute to the pressure. The fix creates its own method for computing T, as if it had been defined by the command:

```
temperature fix-ID all full
```

See the temperature command for details. Note that this is NOT the temperature with ID = *default*. This means you can change the attributes of this fix's temperature (e.g. its degrees-of-freedom) via the temp\_modify command or print the temperature with thermodynamic output via the thermo\_style custom command using the appropriate temp-ID = fix-ID. It also means that changing attributes of the default temperature will have no effect on this fix. Alternatively, you can directly assign a new temperature to the fix via the fix\_modify command. If you do this, note that the kinetic energy derived from T should be consistent with the virial term computed using all atoms. LAMMPS will warn you if you choose to compute temperature on a subset of atoms.

The pressure can be controlled in one of several styles, as specified by the *p-style* argument. Style *xyz* means couple all 3 dimensions together when pressure is computed (isotropic pressure), and dilate/contract the 3 dimensions together.

Styles *xy* or *yz* or *xz* means that the 2 specified dimensions are coupled together, both for pressure computation and for dilation/contraction. The 3rd dimension dilates/contracts independently, using its pressure component as the driving force.

For style *aniso*, all 3 dimensions dilate/contract independently using their individual pressure components as the 3 driving forces.

For any of the styles except *xyz*, any of the independent pressure components (e.g. *z* in *xy*, or any dimension in *aniso*) can have their target pressures (both start and stop values) specified as NULL. This means that no pressure control is applied to that dimension so that the box dimension remains unchanged.

In some cases (e.g. for solids) the pressure (volume) and/or temperature of the system can oscillate undesirably when a Nose/Hoover barostat is applied. The optional *drag* keyword will damp these oscillations, although it alters the Nose/Hoover equations. A value of 0.0 (no drag) leaves the Nose/Hoover formalism unchanged. A non-zero value adds a drag term; the larger the value specified, the greater the damping effect. Performing a short run and monitoring the pressure is the best way to determine if the drag term is working. Typically a value between 0.2 to 2.0 is sufficient to damp oscillations after a few periods.

For all pressure styles, the simulation box stays rectangular in shape. Parinello–Rahman boundary conditions (tilted box) are not implemented in LAMMPS.

For all styles, the *Pdamp* parameter is specified in time units and determines how rapidly the pressure is relaxed. For example, a value of 1000.0 means to relax the temperature in a timespan of (roughly) 1000 time units (tau or fmsec or psec – see the units command).

This fix supports the "fix\_modify" options for *thermo* and *energy*. The former will print the contribution the fix makes to the energy of the system when thermodynamics is printed. The latter will add this contribution to the total potential energy (PotEng) so that energy conservation can be monitored.

### Restrictions:

Any dimension being adjusted by this fix must be periodic. A dimension whose target pressures are specified as NULL can be non-periodic or periodic.

You should not use `fix nvt` with this fix. Instead, use `fix npt` if you want to control both temperature and pressure via Nose/Hoover.

#### Related commands:

`fix nve`, `fix npt`, `fix_modify`

#### Default:

The keyword defaults are `drag = 0.0` and `dilate = all`.

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## fix npt command

#### Syntax:

```
fix ID group-ID npt Tstart Tstop Tdamp p-style args keyword value ...
```

- ID, group-ID are documented in `fix` command
- npt = style name of this fix command
- Tstart, Tstop = desired temperature at start/end of run
- Tdamp = temperature damping parameter (time units)
- p-style = `xyz` or `xy` or `yz` or `xz` or *aniso*

```
xyz args = Pstart Pstop Pdamp
```

```
Pstart, Pstop = desired pressure at start/end of run (pressure units)
```

```
Pdamp = pressure damping parameter (time units)
```

```
xy or yz or xz or aniso args = Px_start Px_stop Py_start Py_stop Pz_start Pz_stop Pdamp
```

```
Px_start, Px_stop, ... = desired pressure in x,y,z at start/end of run (pressure units)
```

```
Pdamp = pressure damping parameter (time units)
```

- zero or more keyword/value pairs may be appended to the args
- keyword = *drag* or *dilate*

```
drag value = drag factor added to barostat/thermostat (0.0 = no drag)
```

```
dilate value = all or partial
```

#### Examples:

```
fix 1 all npt 300.0 300.0 100.0 xyz 0.0 0.0 1000.0
```

```
fix 2 all npt 300.0 300.0 100.0 xz 5.0 5.0 NULL NULL 5.0 5.0 1000.0
```

```
fix 2 all npt 300.0 300.0 100.0 xz 5.0 5.0 NULL NULL 5.0 5.0 1000.0 drag 0.2
```

```
fix 2 water npt 300.0 300.0 100.0 aniso 0.0 0.0 0.0 0.0 NULL NULL 1000.0 dilate partial
```

#### Description:

Perform constant NPT integration to update positions and velocities each timestep for atoms in the group using a Nose/Hoover temperature thermostat and Nose/Hoover pressure barostat. P is pressure; T is temperature. This creates a system trajectory consistent with the isothermal–isobaric ensemble.

The desired temperature at each timestep is a ramped value during the run from  $T_{start}$  to  $T_{stop}$ . The  $T_{damp}$  parameter is specified in time units and determines how rapidly the temperature is relaxed. For example, a value of 100.0 means to relax the temperature in a timespan of (roughly) 100 time units (tau or fmsec or psec – see the units command).

The atoms in the fix group are the only ones whose velocities and positions are updated by the velocity/position update portion of the NPT integration.

Regardless of what atoms are in the fix group, a global pressure is computed for all atoms. Similarly, when the size of the simulation box is changed, all atoms are re-scaled to new positions, unless the keyword *dilate* is specified with a value of *partial*, in which case only the atoms in the fix group are re-scaled. The latter can be useful for leaving the coordinates of atoms in a solid substrate unchanged and controlling the pressure of a surrounding fluid.

This fix computes a temperature each timestep, to contribute to the pressure. The fix creates its own method for computing T, as if it had been defined by the command:

```
temperature fix-ID all full
```

See the temperature command for details. Note that this is NOT the temperature with ID = *default*. This means you can change the attributes of this fix's temperature (e.g. its degrees-of-freedom) via the temp\_modify command or print the temperature with thermodynamic output via the thermo\_style custom command using the appropriate temp-ID = fix-ID. It also means that changing attributes of the default temperature will have no effect on this fix. Alternatively, you can directly assign a new temperature to the fix via the fix\_modify command. If you do this, note that the kinetic energy derived from T should be consistent with the virial term computed using all atoms. LAMMPS will warn you if you choose to compute temperature on a subset of atoms.

The pressure can be controlled in one of several styles, as specified by the *p-style* argument. Style *xyz* means couple all 3 dimensions together when pressure is computed (isotropic pressure), and dilate/contract the 3 dimensions together.

Styles *xy* or *yz* or *xz* means that the 2 specified dimensions are coupled together, both for pressure computation and for dilation/contraction. The 3rd dimension dilates/contracts independently, using its pressure component as the driving force.

For style *aniso*, all 3 dimensions dilate/contract independently using their individual pressure components as the 3 driving forces.

For any of the styles except *xyz*, any of the independent pressure components (e.g. z in *xy*, or any dimension in *aniso*) can have their target pressures (both start and stop values) specified as NULL. This means that no pressure control is applied to that dimension so that the box dimension remains unchanged.

In some cases (e.g. for solids) the pressure (volume) and/or temperature of the system can oscillate undesirably when a Nose/Hoover barostat and thermostat is applied. The optional *drag* keyword will damp these oscillations, although it alters the Nose/Hoover equations. A value of 0.0 (no drag) leaves the Nose/Hoover formalism unchanged. A non-zero value adds a drag term; the larger the value specified, the greater the damping effect. Performing a short run and monitoring the pressure and temperature is the best way to determine if the drag term is working. Typically a value between 0.2 to 2.0 is sufficient to damp oscillations after a few periods.

For all pressure styles, the simulation box stays rectangular in shape. Parinello–Rahman boundary conditions (tilted box) are not implemented in LAMMPS.

For all styles, the *Pdamp* parameter operates like the *Tdamp* parameter, determining the time scale on which pressure is relaxed.

This fix supports the fix\_modify options for *thermo* and *energy*. The former will print the contribution the fix makes to the energy of the system when thermodynamics is printed. The latter will add this contribution to the total potential energy (PotEng) so that energy conservation can be monitored.

#### Restrictions:

Any dimension being adjusted by this fix must be periodic. A dimension whose target pressures are specified as NULL can be non-periodic or periodic.

#### Related commands:

fix nve, fix nvt, fix nph, fix\_modify

#### Default:

The keyword defaults are drag = 0.0 and dilate = all.

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## fix nve command

#### Syntax:

```
fix ID group-ID nve
```

- ID, group-ID are documented in fix command
- nve = style name of this fix command

#### Examples:

```
fix 1 all nve
```

#### Description:

Perform constant NVE updates of position and velocity for atoms in the group each timestep. V is volume; E is energy. This creates a system trajectory consistent with the microcanonical ensemble.

**Restrictions:** none

#### Related commands:

fix nvt, fix npt

**Default:** none

## fix nve/gran command

### Syntax:

```
fix ID group-ID nve/gran
```

- ID, group-ID are documented in [fix](#) command
- nve/gran = style name of this fix command

### Examples:

```
fix 1 all nve/gran
```

### Description:

Perform constant NVE updates each timestep on a group of atoms of atom style granular. V is volume; E is energy. Granular atoms store rotational information as well as position and velocity, so this integrator updates translational and rotational degrees of freedom due to forces and torques.

**Restrictions:** none

Can only be used if LAMMPS was built with the "granular" package. Can only be used with atom\_style granular.

### Related commands:

[atom\\_style granular](#)

**Default:** none

## fix nvt command

### Syntax:

```
fix ID group-ID nvt Tstart Tstop Tdamp keyword value ...
```

- ID, group-ID are documented in [fix](#) command
- nvt = style name of this fix command
- Tstart, Tstop = desired temperature at start/end of run
- Tdamp = temperature damping parameter (time units)
- zero or more keyword/value pairs may be appended to the args
- keyword = *drag*

*drag* value = drag factor added to thermostat (0.0 = no drag)

### Examples:

fix nve/gran command



```
fix 1 all nvt 300.0 300.0 100.0
fix 1 all nvt 300.0 300.0 100.0 drag 0.2
```

### Description:

Perform constant NVT integration to update positions and velocities each timestep for atoms in the group using a Nose/Hoover temperature thermostat. V is volume; T is temperature. This creates a system trajectory consistent with the canonical ensemble.

The desired temperature at each timestep is a ramped value during the run from  $T_{start}$  to  $T_{stop}$ . The  $T_{damp}$  parameter is specified in time units and determines how rapidly the temperature is relaxed. For example, a value of 100.0 means to relax the temperature in a timespan of (roughly) 100 time units (tau or fmsec or psec – see the units command).

In some cases (e.g. for solids) the temperature of the system can oscillate undesirably when a Nose/Hoover thermostat is applied. The optional *drag* keyword will damp these oscillations, although it alters the Nose/Hoover equations. A value of 0.0 (no drag) leaves the Nose/Hoover formalism unchanged. A non-zero value adds a drag term; the larger the value specified, the greater the damping effect. Performing a short run and monitoring the temperature is the best way to determine if the drag term is working. Typically a value between 0.2 to 2.0 is sufficient to damp oscillations after a few periods.

This fix computes a temperature each timestep. The fix creates its own method for computing T, as if it had been defined by the command:

```
temperature fix-ID group-ID full
```

See the temperature command for details. Note that this is NOT the temperature with ID = *default*. This means you can change the attributes of this fix's temperature (e.g. its degrees-of-freedom) via the temp\_modify command or print the temperature with thermodynamic output via the thermo\_style custom command using the appropriate temp-ID = fix-ID. It also means that changing attributes of the default temperature will have no effect on this fix. Alternatively, you can directly assign a new temperature to the fix via the fix\_modify command.

This fix supports the fix\_modify options for *thermo* and *energy*. The former will print the contribution the fix makes to the energy of the system when thermodynamics is printed. The latter will add this contribution to the total potential energy (PotEng) so that energy conservation can be monitored.

**Restrictions:** none

**Related commands:**

fix nve, fix npt, fix temp/rescale, fix langevin, fix\_modify, temperature

**Default:**

The keyword defaults are drag = 0.0.

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## fix orient/fcc command

```
fix ID group-ID orient/fcc nstats dir alat dE cutlo cuthi file0 file1
```

- ID, group-ID are documented in [fix](#) command
- nstats = print stats every this many steps, 0 = never
- dir = 0/1 for which crystal is used as reference
- alat = fcc cubic lattice constant (distance units)
- dE = energy added to each atom (energy units)
- cutlo,cuthi = values between 0.0 and 1.0, cutlo < cuthi
- file0,file1 = files that specify orientation of each grain

### Examples:

```
fix gb all orient/fcc 0 1 4.032008 0.001 0.25 0.75 xi.vec chi.vec
```

### Description:

The fix applies an orientation-dependent force to atoms near a planar grain boundary which can be used to induce grain boundary migration (in the direction perpendicular to the grain boundary plane). The motivation and explanation of this force and its application are described in [\(Janssens\)](#). The force is only applied to atoms in the fix group.

The basic idea is that atoms in one grain (on one side of the boundary) have a potential energy dE added to them. Atoms in the other grain have 0.0 potential energy added. Atoms near the boundary (whose neighbor environment is intermediate between the two grain orientations) have an energy between 0.0 and dE added. This creates an effective driving force to reduce the potential energy of atoms near the boundary by pushing them towards one of the grain orientations. For dir = 1 and dE > 0, the boundary will thus move so that the grain described by file0 grows and the grain described by file1 shrinks. Thus this fix is designed for simulations of two-grain systems, either with one grain boundary and free surfaces parallel to the boundary, or a system with periodic boundary conditions and two equal and opposite grain boundaries. In either case, the entire system can displace during the simulation, and such motion should be accounted for in measuring the grain boundary velocity.

The potential energy added to atom I is given by these formulas

$$\xi_i = \sum_{j=1}^{12} |\mathbf{r}_j - \mathbf{r}_j^I| \quad (1)$$

$$\xi_{IJ} = \sum_{j=1}^{12} |\mathbf{r}_j^I - \mathbf{r}_j^J| \quad (2)$$

$$\xi_{\text{low}} = \text{cutlo} \xi_{IJ} \quad (3)$$

$$\xi_{\text{high}} = \text{cuthi} \xi_{IJ} \quad (4)$$

$$\omega_i = \frac{\pi}{2} \frac{\xi_i - \xi_{\text{low}}}{\xi_{\text{high}} - \xi_{\text{low}}} \quad (5)$$

$$\begin{aligned} u_i &= 0 && \text{for } \xi_i < \xi_{\text{low}} \\ &= dE \frac{1 - \cos(2\omega_i)}{2} && \text{for } \xi_{\text{low}} < \xi_i < \xi_{\text{high}} \\ &= dE && \text{for } \xi_{\text{high}} < \xi_i \end{aligned} \quad (6)$$

which are fully explained in [\(Janssens\)](#). The order parameter  $\xi_i$  for atom  $I$  in equation (1) is a sum over the 12 nearest neighbors of atom  $I$ .  $\mathbf{r}_j$  is the vector from atom  $I$  to its neighbor  $J$ , and  $\mathbf{r}_j^I$  is a vector in the reference (perfect) crystal. That is, if  $\text{dir} = 0/1$ , then  $\mathbf{r}_j^I$  is a vector to an atom coord from file 0/1. Equation (2) gives the expected value of the order parameter  $\xi_{IJ}$  in the other grain.  $\text{hi}$  and  $\text{lo}$  cutoffs are defined in equations (3) and (4), using the input parameters *cutlo* and *cuthi* as thresholds to avoid adding grain boundary energy when the deviation in the order parameter from 0 or 1 is small (e.g. due to thermal fluctuations in a perfect crystal). The added potential energy  $U_i$  for atom  $I$  is given in equation (6) where it is interpolated between 0 and  $dE$  using the two threshold  $\xi_i$  values and the  $W_i$  value of equation (5).

The derivative of this energy expression gives the force on each atom which thus depends on the orientation of its neighbors relative to the 2 grain orientations. Only atoms near the grain boundary feel a net force which tends to drive them to one of the two grain orientations.

In equation (1), the reference vector used for each neighbor is the reference vector closest to the actual neighbor position. This means it is possible two different neighbors will use the same reference vector. In such cases, the atom in question is far from a perfect orientation and will likely receive the full  $dE$  addition, so the effect of duplicate reference vector usage is small.

The *dir* parameter determines which grain wants to grow at the expense of the other. A value of 0 means the first grain will shrink; a value of 1 means it will grow. This assumes that  $dE$  is positive. The reverse will be true if  $dE$  is negative.

The *alat* parameter is the cubic lattice constant for the fcc material and is only used to compute a cutoff distance of  $1.57 * \text{alat} / \sqrt{2}$  for finding the 12 nearest neighbors of each atom (which should be valid for an fcc crystal). A longer/shorter cutoff can be imposed by adjusting *alat*. If a particular atom has less than 12 neighbors within the cutoff, the order parameter of equation (1) is effectively multiplied by 12 divided by the actual number of neighbors within the cutoff.

The *dE* parameter is the maximum amount of additional energy added to each atom in the grain which wants to shrink.

The *cutlo* and *cuthi* parameters are used to reduce the force added to bulk atoms in each grain far away from the boundary. An atom in the bulk surrounded by neighbors at the ideal grain orientation would compute an order parameter of 0 or 1 and have no force added. However, thermal vibrations in the solid will cause the order parameters to be greater than 0 or less than 1. The cutoff parameters mask this effect, allowing forces to only be added to atoms with order-parameters between the cutoff values.

*File0* and *file1* are filenames for the two grains which each contain 6 vectors (6 lines with 3 values per line) which specify the grain orientations. Each vector is a displacement from a central atom (0,0,0) to a nearest neighbor atom in an fcc lattice at the proper orientation. The vector lengths should all be identical since an fcc lattice has a coordination number of 12. Only 6 are listed due to symmetry, so the list must include one from each pair of equal-and-opposite neighbors. A pair of orientation files for a Sigma=5 tilt boundary are show below.

This fix supports the fix\_modify options for *thermo* and *energy*. The former will print the contribution the fix makes to the energy of the system when thermodynamics is printed. The latter will add this contribution to the total potential energy (PotEng).

### Restrictions:

This fix should only be used with fcc lattices.

### Related commands:

fix\_modify

**Default:** none

---

**(Janssens)** Janssens, Olmsted, Holm, Foiles, Plimpton, Derlet, Nature Materials, 5, 124–127 (2006).

---

For illustration purposes, here are example files that specify a Sigma=5 tilt boundary. This is for a lattice constant of 3.5706 Angs.

file0:

```

0.798410432046075    1.7853000000000000    1.596820864092150
-0.798410432046075    1.7853000000000000    -1.596820864092150
2.395231296138225    0.0000000000000000    0.798410432046075
0.798410432046075    0.0000000000000000    -2.395231296138225
1.596820864092150    1.7853000000000000    -0.798410432046075
1.596820864092150    -1.7853000000000000    -0.798410432046075
```

file1:

```

-0.798410432046075    1.7853000000000000    1.596820864092150
0.798410432046075    1.7853000000000000    -1.596820864092150
0.798410432046075    0.0000000000000000    2.395231296138225
2.395231296138225    0.0000000000000000    -0.798410432046075
1.596820864092150    1.7853000000000000    0.798410432046075
1.596820864092150    -1.7853000000000000    0.798410432046075
```

## fix planeforce command

### Syntax:

```
fix ID group-ID planeforce x y z
```

- ID, group-ID are documented in [fix](#) command
- lineforce = style name of this fix command
- x y z = 3-vector that is normal to the plane

### Examples:

```
fix hold boundary planeforce 1.0 0.0 0.0
```

### Description:

Adjust the forces on each atom in the group so that it's motion will be in the plane specified by the normal vector (x,y,z). This is done by subtracting out components of force perpendicular to the plane.

If the initial velocity of the atom is 0.0 (or in the plane), then it should continue to move in the plane thereafter.

**Restrictions:** none

**Related commands:**

[fix lineforce](#)

**Default:** none

## fix poems

### Syntax:

```
fix ID group-ID poems keyword values
```

- ID, group-ID are documented in [fix](#) command
- poems = style name of this fix command
- keyword = *group* or *file* or *molecule*

```
group values = list of group IDs
molecule values = none
file values = filename
```

### Examples:

```
fix 3 fluid poems group clump1 clump2 clump3
```

fix 3 fluid poems file cluster.list

## Description:

Treats one or more sets of atoms as coupled rigid bodies. This means that each timestep the total force and torque on each rigid body is computed and the coordinates and velocities of the atoms are updated so that the collection of bodies move as a coupled set. This can be useful for treating a large biomolecule as a collection of connected, coarse-grained particles.

The coupling, associated motion constraints, and time integration is performed by the software package Parallelizable Open source Efficient Multibody Software (POEMS) which computes the constrained rigid-body motion of articulated (jointed) multibody systems (Anderson). POEMS was written and is distributed by Prof Kurt Anderson, his graduate student Rudranarayan Mukherjee, and other members of his group at Rensselaer Polytechnic Institute (RPI). Rudranarayan developed the LAMMPS/POEMS interface. For copyright information on POEMS and other details, please refer to the documents in the poems directory distributed with LAMMPS.

This fix updates the positions and velocities of the rigid atoms with a constant-energy time integration, so you should not update the same atoms via other fixes (e.g. nve, nvt, npt, temp/rescale, langevin).

Each body must have a non-degenerate inertia tensor, which means it must contain at least 3 non-collinear atoms. Which atoms are in which bodies can be defined via several options.

For option *group*, each of the listed groups is treated as a rigid body. Note that only atoms that are also in the fix group are included in each rigid body.

For option *molecule*, each set of atoms in the group with a different molecule ID is treated as a rigid body.

For option *file*, sets of atoms are read from the specified file and each set is treated as a rigid body. Each line of the file specifies a rigid body in the following format:

ID type atom1-ID atom2-ID atom3-ID ...

ID as an integer from 1 to M (the number of rigid bodies). Type is any integer; it is not used by the fix poems command. The remaining arguments are IDs of atoms in the rigid body, each typically from 1 to N (the number of atoms in the system). Only atoms that are also in the fix group are included in each rigid body. Blank lines and lines that begin with '#' are skipped.

A connection between a pair of rigid bodies is inferred if one atom is common to both bodies. The POEMS solver treats that atom as a spherical joint with 3 degrees of freedom. Currently, a collection of bodies can only be connected by joints as a linear chain. The entire collection of rigid bodies can represent one or more chains. Other connection topologies (tree, ring) are not allowed, but will be added later. Note that if no joints exist, it is more efficient to use the fix rigid command to simulate the system.

When the poems fix is defined, it will print out statistics on the total # of clusters, bodies, joints, atoms involved. A cluster in this context means a set of rigid bodies connected by joints.

For computational efficiency, you should turn off pairwise and bond interactions within each rigid body, as they no longer contribute to the motion. The "neigh\_modify exclude" and "delete\_bonds" commands can be used to do this if each rigid body is a group.

For computational efficiency, you should only define one fix poems which includes all the desired rigid bodies. LAMMPS will allow multiple poems fixes to be defined, but it is more expensive.

The degrees-of-freedom removed by coupled rigid bodies are accounted for in temperature and pressure computations. Similarly, the rigid body contribution to the pressure virial is also accounted for. The latter is only correct if forces within the bodies have been turned off, and there is only a single fix poems defined.

Restrictions:

Can only be used if LAMMPS was built with the "poems" package.

Related commands:

fix rigid, delete\_bonds, neigh\_modify exclude

Default: none

---

:link(Anderson) (**Anderson**) Anderson, Mukherjee, Critchley, Ziegler, and Lipton "POEMS: Parallelizable Open-source Efficient Multibody Software ", Engineering With Computers (2006). ([link to paper](#))

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## fix print command

### Syntax:

```
fix ID group-ID print N string
```

- ID, group-ID are documented in fix command
- print = style name of this fix command
- N = print every N steps
- string = text string to print with optional variable names

### Examples:

```
fix extra all print 100 "Coords of marker atom = $x $y $z"
```

### Description:

Print a text string to the screen and logfile every N steps during a simulation run. This can be used for diagnostic purposes or even as a debugging tool to monitor some quantity during a run. The text string must be a single argument, so it should be enclosed in double quotes if it is more than one word. If it contains variables (\$a thru \$z) it must be enclosed in double quotes to insure they are not evaluated when the input script is read, but will instead be evaluated when the string is printed.

See the variable command for a description of *equal* style variables which are the most useful ones to use with the fix print command, since they are evaluated afresh each timestep that the fix print line is output.

Note that if *equal*-style variables are used in the print line which contain thermo style custom keywords for potential energy such as pe, eng, evdwl, ebond, etc, they will only be up-to-date on timesteps where

thermodynamics are computed. Hence, if you output thermodynamics every 100 steps, but issue a fix print command with N = 2 that contains such a variable, the printed value will only be current on timesteps that are a multiple of 100. This is because the potential functions in LAMMPS (pairwise, bond, etc) only compute energies on timesteps when thermodynamic output is being performed.

**Restrictions:** none

**Related commands:**

[variable](#), [print](#)

**Default:** none

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---

## fix rdf command

### Syntax:

```
fix ID group-ID rdf N file Nbin itype1 jtype1 itype2 jtype2 ...
```

- ID, group-ID are documented in [fix](#) command
- rdf = style name of this fix command
- N = compute radial distribution function (RDF) every this many timesteps
- file = filename to write radial distribution function info to
- Nbin = number of RDF bins
- itypeN = central atom type for RDF pair N
- jtypeN = distribution atom type for RDF pair N

### Examples:

```
fix 1 all rdf 500 rdf.out 100 1 1
fix 1 fluid rdf 10000 rdf.out 100 1 1 1 2 2 1 2 2
```

### Description:

Compute the radial distribution function (RDF), also known as  $g(r)$ , and coordination number every N steps. The RDF for each specified atom type pair is histogrammed in Nbin bins from distance 0 to  $R_c$ , where  $R_c$  = the maximum force cutoff for any pair of atom types. An atom pair only contributes to the RDF if

- both atoms are in the fix group
- the distance between them is within the maximum force cutoff
- their interaction is stored in the neighbor list

Bonded atoms (1–2, 1–3, 1–4 interactions within a molecular topology) with a pairwise weighting factor of 0.0 are not included in the RDF; pairs with a non-zero weighting factor are included. The weighting factor is set by the [special\\_bonds](#) command.

The RDF statistics for each timestep are written to the specified file, as are the RDF values averaged over all timesteps.



## Restrictions:

The RDF is not computed for distances longer than the force cutoff, since processors (in parallel) don't know atom coordinates for atoms further away than that distance. If you want an RDF for larger  $r$ , you'll need to post-process a dump file.

## Related commands:

[pair\\_style](#)

**Default:** none

---

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---

## fix rigid

### Syntax:

```
fix ID group-ID rigid keyword values
```

- ID, group-ID are documented in [fix](#) command
- rigid = style name of this fix command
- keyword = *single* or *molecule* or *group*

```
single values = none
molecule values = none
group values = list of group IDs
```

### Examples:

```
fix 1 clump rigid single
fix 1 polychains rigid molecule
fix 2 fluid rigid group clump1 clump2 clump3
```

### Description:

Treat one or more sets of atoms as an independent rigid body. This means that each timestep the total force and torque on each rigid body is computed and the coordinates and velocities of the atoms in each body are updated so that they move as a rigid body. This can be useful for freezing one or more portions of a large biomolecule, or for simulating a system of colloidal particles.

This fix updates the positions and velocities of the rigid atoms with a constant-energy time integration, so you should not update the same atoms via other fixes (e.g. nve, nvt, npt, temp/rescale, langevin).

Each body must have two or more atoms. Which atoms are in which bodies can be defined via several options.

For option *single* the entire group of atoms is treated as one rigid body.

For option *molecule*, each set of atoms in the group with a different molecule ID is treated as a rigid body.

For option *group*, each of the listed groups is treated as a separate rigid body. Note that only atoms that are also in the *fix* group are included in each rigid body.

For computational efficiency, you should also turn off pairwise and bond interactions within each rigid body, as they no longer contribute to the motion. The *neigh\_modify exclude* and *delete\_bonds* commands are used to do this.

For computational efficiency, you should define one *fix rigid* which includes all the desired rigid bodies. LAMMPS will allow multiple rigid fixes to be defined, but it is more expensive.

The degrees-of-freedom removed by rigid bodies are accounted for in temperature and pressure computations. Similarly, the rigid body contribution to the pressure virial is also accounted for. The latter is only correct if forces within the bodies have been turned off, and there is only a single *fix rigid* defined.

Note that this *fix* uses constant-energy integration, so you need to impose additional constraints to control the temperature of an ensemble of rigid bodies. You can use *fix langevin* for this purpose to treat the system as effectively immersed in an implicit solvent, i.e. a Brownian dynamics model. Or you can thermostat the atoms of an explicit solvent directly.

#### Restrictions:

This *fix* performs an MPI\_Allreduce each timestep that is proportional in length to the number of rigid bodies. Hence it will not scale well in parallel if large numbers of rigid bodies are simulated.

If the atoms in a single rigid body initially straddle a periodic boundary, the input data file must define the image flags for each atom correctly, so that LAMMPS can "unwrap" the atoms into a valid rigid body.

#### Related commands:

*delete\_bonds*, *neigh\_modify exclude*

**Default:** none

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## fix setforce command

#### Syntax:

```
fix ID group-ID setforce fx fy fz
```

- ID, group-ID are documented in *fix* command
- setforce = style name of this *fix* command
- fx,fy,fz = force component values

#### Examples:

```
fix freeze indenter setforce 0.0 0.0 0.0
fix 2 edge setforce NULL 0.0 0.0
```

#### Description:

*fix setforce* command

Set each component of force on each atom in the group to the specified values  $f_x, f_y, f_z$ . This erases all previously computed forces on the atom, though additional fixes could add new forces. This command can be used to freeze certain atoms in the simulation by zeroing their force, assuming their initial velocity zero.

Any of the  $f_x, f_y, f_z$  values can be specified as NULL which means do not alter the force component in that dimension.

**Restrictions:** none

**Related commands:**

[fix addforce](#), [fix aveforce](#)

**Default:** none

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## fix shake style

### Syntax:

```
fix ID group-ID shake tol iter N keyword values ...
```

- ID, group-ID are documented in [fix](#) command
- shake = style name of this fix command
- tol = accuracy tolerance of SHAKE solution
- iter = max # of iterations in each SHAKE solution
- N = print SHAKE statistics every this many timesteps (0 = never)
- one or more keyword/value pairs are appended
- keyword = *b* or *a* or *t* or *m*

```
b values = one or more bond types
a values = one or more angle types
t values = one or more atom types
m value  = one or more mass values
```

### Examples:

```
fix 1 sub shake 0.0001 20 10 b 4 19 a 3 5 2
fix 1 sub shake 0.0001 20 10 t 5 6 m 1.0 a 31
```

### Description:

Apply bond and angle constraints to specified bonds and angles in the simulation. This typically enables a longer timestep.

Each timestep the specified bonds and angles are reset to their equilibrium lengths and angular values via the well-known SHAKE algorithm. This is done by applying an additional constraint force so that the new positions preserve the desired atom separations. The equations for the additional force are solved via an iterative method that typically converges to an accurate solution in a few iterations. The desired tolerance (e.g.  $1.0\text{e-}4 = 1$  part in 10000) and maximum # of iterations are specified as arguments. Setting the N argument will print statistics to the screen and log file about regarding the lengths of bonds and angles that are being

constrained. Small delta values mean SHAKE is doing a good job.

In LAMMPS, only small clusters of atoms can be constrained. This is so the constraint calculation for a cluster can be performed by a single processor, to enable good parallel performance. A cluster is defined as a central atom connected to others in the cluster by constrained bonds. LAMMPS allows for the following kinds of clusters to be constrained: one central atom bonded to 1 or 2 or 3 atoms, or one central atom bonded to 2 others and the angle between the 3 atoms also constrained. This means water molecules or CH<sub>2</sub> or CH<sub>3</sub> groups may be constrained, but not all the C–C backbone bonds of a long polymer chain.

The *b* keyword lists bond types that will be constrained. The *t* keyword lists atom types. All bonds connected to an atom of the specified type will be constrained. The *m* keyword lists atom masses. All bonds connected to atoms of the specified masses will be constrained (within a fudge factor of MASSDELTA specified in fix\_shake.cpp). The *a* keyword lists angle types. If both bonds in the angle are constrained then the angle will also be constrained if its type is in the list.

For all keywords, a particular bond is only constrained if both atoms in the bond are in the group specified with the SHAKE fix.

The degrees-of-freedom removed by SHAKE bonds and angles are accounted for in temperature and pressure computations. Similarly, the SHAKE contribution to the pressure virial is also accounted for.

### Restrictions:

For computational efficiency, there can only be one shake fix defined in a simulation.

If you use a tolerance that is too large or a max-iteration count that is too small, the constraints will not be enforced very strongly, which can lead to poor energy conservation. You can test for this in your system by running a constant NVE simulation with a particular set of SHAKE parameters and monitoring the energy versus time.

**Related commands:** none

**Default:** none

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## fix spring command

### Syntax:

```
fix ID group-ID spring keyword values
```

- ID, group-ID are documented in [fix](#) command
- spring = style name of this fix command
- keyword = *tether* or *couple*

```
tether values = K x y z R0
    K = spring constant (force/distance units)
    x,y,z = point to which spring is tethered
    R0 = equilibrium distance from tether point (distance units)
couple values = group-ID1 group-ID2 K x y z R0
    group-ID1,group-ID2 = two groups to couple together with a spring
```

K = spring constant (force/distance units)  
x,y,z = direction of spring  
R0 = equilibrium distance of spring (distance units)

### Examples:

```
fix pull ligand spring tether 50.0 0.0 0.0 0.0 0.0
fix pull ligand spring tether 50.0 0.0 0.0 0.0 5.0
fix pull ligand spring tether 50.0 NULL NULL 2.0 3.0
fix 5 lipids spring couple bilayer1 bilayer2 100.0 NULL NULL 10.0 0.0
fix longitudinal all spring couple pore ion 100.0 NULL NULL -20.0 0.0
fix radial all spring couple pore ion 100.0 0.0 0.0 NULL 5.0
```

### Description:

Apply a spring force to a group of atoms or between two groups of atoms. This is useful for applying an umbrella force to a small molecule or lightly tethering a large group of atoms (e.g. all the solvent or a large molecule) to the center of the simulation box so that it doesn't wander away over the course of a long simulation. It can also be used to hold the centers of mass of two groups of atoms at a given distance or orientation with respect to each other.

The *tether* style attaches a spring between a fixed point  $x,y,z$  and the center of mass of the fix group of atoms. The equilibrium position of the spring is  $R0$ . At each timestep the distance  $R$  from the center of mass of the group of atoms to the tethering point is computed, taking account of wrap-around in a periodic simulation box. A restoring force of magnitude  $K (R - R0) M_i / M$  is applied to each atom in the group where  $K$  is the spring constant,  $M_i$  is the mass of the atom, and  $M$  is the total mass of all atoms in the group. Note that  $K$  thus represents the total force on the group of atoms, not a per-atom force.

The *couple* style links two groups of atoms together. Only atoms that are also in the fix group are considered to be part of either of the groups. The groups are coupled together by a spring that is at equilibrium when the two groups are displaced by a vector  $x,y,z$  with respect to each other and at a distance  $R0$  from that displacement. Note that  $x,y,z$  is the equilibrium displacement of group 2 relative to group 1. Thus (1,1,0) is a different spring than (-1,-1,0). When the relative positions and distance between the two groups are not in equilibrium, the same spring force described above is applied to atoms in each of the two groups.

For both the *tether* and *couple* styles, any of the  $x,y,z$  values can be specified as NULL which means do not include that dimension in the distance calculation or force application.

The first example above pulls the ligand towards the point (0,0,0). The second example holds the ligand near the surface of a sphere of radius 5 around the point (0,0,0). The third example holds the ligand a distance 3 away from the  $z=2$  plane (on either side).

The fourth example holds 2 bilayers a distance 10 apart in  $z$ . For the last two examples, imagine a pore (a slab of atoms with a cylindrical hole cut out) oriented with the pore axis along  $z$ , and an ion moving within the pore. The fifth example holds the ion a distance of -20 below the  $z = 0$  center plane of the pore (umbrella sampling). The last example holds the ion a distance 5 away from the pore axis (assuming the center-of-mass of the pore in  $x,y$  is the pore axis).

**Restrictions:** none

**Related commands:**

[fix drag](#), [fix spring/self](#), [fix spring/rg](#)

**Default:** none

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---

## fix spring/rg command

### Syntax:

```
fix ID group-ID spring/rg K RG0
```

- ID, group-ID are documented in [fix](#) command
- spring/rg = style name of this fix command
- K = harmonic force constant (force/distance units)
- RG0 = target radius of gyration to constrain to (distance units)

if RG0 = NULL, use the current RG as the target value

### Examples:

```
fix 1 protein spring/rg 5.0 10.0  
fix 2 micelle spring/rg 5.0 NULL
```

### Description:

Apply a harmonic restraining force to atoms in the group to affect their central moment about the center of mass (radius of gyration). This fix is useful to encourage a protein or polymer to fold/unfold and also when sampling along the radius of gyration as a reaction coordinate (i.e. for protein folding).

The radius of gyration is defined as RG in the first formula. The energy of the constraint and associated force on each atom is given by the second and third formulas, when the group is at a different RG than the target value RG0.

$$R_G^2 = \frac{1}{M} \sum_i^N m_i \left( x_i - \frac{1}{M} \sum_j^N m_j x_j \right)^2$$

$$E = K (R_G - R_{G0})^2$$

$$F_i = 2K \frac{m_i}{M} \left( 1 - \frac{R_{G0}}{R_G} \right) \left( x_i - \frac{1}{M} \sum_j^N m_j x_j \right)$$

The (xi – center-of-mass) term is computed taking into account periodic boundary conditions, m\_i is the mass of the atom, and M is the mass of the entire group. Note that K is thus a force constant for the aggregate force on the group of atoms, not a per-atom force.

If RG0 is specified as NULL, then the RG of the group is computed at the time the fix is specified, and that value is used as the target.

**Restrictions:** none

**Related commands:**

[fix spring](#), [fix spring/self](#)

**Default:** none

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## fix spring/self command

**Syntax:**

```
fix ID group-ID spring/self K
```

- ID, group-ID are documented in [fix](#) command
- spring/self = style name of this fix command
- K = spring constant (force/distance units)

**Examples:**

```
fix tether boundary-atoms spring/self 10.0
```

**Description:**

Apply a spring force independently to each atom in the group to tether it to its initial position. The initial position for each atom is its location at the time the fix command was issued. At each timestep, the magnitude of the force on each atom is  $-Kr$ , where  $r$  is the displacement of the atom from its current position to its initial position.

**Restrictions:** none

**Related commands:**

[fix drag](#), [fix spring](#)

**Default:** none

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## fix temp/rescale command

**Syntax:**

```
fix ID group-ID temp/rescale N Tstart Tstop window fraction keyword values ...
```

- ID, group-ID are documented in [fix](#) command
- temp/rescale = style name of this fix command
- N = perform rescaling every N steps

- $T_{start}, T_{stop}$  = desired temperature at start/end of run (temperature units)
- *window* = only rescale if temperature is outside this window (temperature units)
- *fraction* = rescale to target temperature by this fraction
- zero or more keyword/value pairs may be appended to the args

```
keyword = region
region values = region-ID
region-ID = ID of region to apply rescaling to
```

### Examples:

```
fix 3 flow temp/rescale 100 1.0 1.1 0.02 0.5
fix 3 boundary temp/rescale 1 1.0 1.5 0.05 1.0 region edge
```

### Description:

Reset the temperature of a group of atoms by explicitly rescaling their velocities.

Rescaling is performed every  $N$  timesteps. The target temperature is a ramped value between the  $T_{start}$  and  $T_{stop}$  temperatures at the beginning and end of the run. Rescaling is only performed if the difference between the current and desired temperatures is greater than the *window* value. The amount of rescaling that is applied is a *fraction* (from 0.0 to 1.0) of the difference between the actual and desired temperature. E.g. if *fraction* = 1.0, the temperature is reset to exactly the desired value.

The keyword *region* applies the fix only to atoms that are in the specified geometric region (and in the fix group). Since atoms can enter/leave a region, this test is performed each timestep.

This fix computes a temperature each timestep. The fix creates its own method for computing  $T$ , as if it had been defined by one of these commands:

```
temperature fix-ID group-ID full
temperature fix-ID group-ID region region-ID
```

Which is used depends on whether a region was specified with the fix. See the [temperature](#) command for details. Note that this is NOT the temperature with ID = *default*. This means you can change the attributes of this fix's temperature (e.g. its degrees-of-freedom) via the [temp\\_modify](#) command or print the temperature with thermodynamic output via the [thermo\\_style custom](#) command using the appropriate temp-ID = fix-ID. It also means that changing attributes of the default temperature will have no effect on this fix. Alternatively, you can directly assign a new temperature to the fix via the [fix\\_modify](#) command. For consistency, if using the keyword *region*, the temperature you assign should also be of style *region*.

A temp/rescale fix does not update the coordinates of its atoms. It is normally used with a fix of style *nve* that does that. A temp/rescale fix should not normally be used on atoms that also have their temperature controlled by another fix – e.g. a [nvt](#) or [langevin](#) fix.

This fix supports the [fix\\_modify](#) options for *thermo* and *energy*. The former will print the contribution the fix makes to the energy of the system when thermodynamics is printed. The latter will add this contribution to the total potential energy (PotEng) so that energy conservation can be monitored.

**Restrictions:** none

**Related commands:**

fix spring/self command



[fix langevin](#), [fix nvt](#), [fix modify](#)

**Default:** none

## fix tmd command

### Syntax:

```
fix ID group-ID tmd rho_final file1 N file2
```

- ID, group-ID are documented in [fix](#) command
- tmd = style name of this fix command
- rho\_final = desired value of rho at the end of the run (distance units)
- file1 = filename to read target structure from
- N = dump TMD statistics every this many timesteps, 0 = no dump
- file2 = filename to write TMD statistics to (only needed if N > 0)

### Examples:

```
fix 1 all nve
fix 2 tmdatoms tmd 1.0 target_file 100 tmd_dump_file
```

### Description:

Perform targeted molecular dynamics (TMD) on a group of atoms. A holonomic constraint is used to force the atoms to move towards (or away from) the target configuration. The parameter "rho" is monotonically decreased (or increased) from its initial value to rho\_final at the end of the run. Rho has distance units and is a measure of the root-mean-squared distance (RMSD) between the current configuration of the atoms in the group and the target coordinates listed in file1. Thus a value of rho\_final = 0.0 means move the atoms all the way to the final structure during the course of the run.

The format of the target file1 is as follows:

```
0.0 25.0 xlo xhi
0.0 25.0 ylo yhi
0.0 25.0 zlo zhi
125      24.97311    1.69005      23.46956 0 0 -1
126      1.94691     2.79640      1.92799 1 0 0
127      0.15906     3.46099      0.79121 1 0 0
...
```

The first 3 lines may or may not be needed, depending on the format of the atoms to follow. If image flags are included with the atoms, the 1st 3 lo/hi lines must appear in the file. If image flags are not included, the 1st 3 lines should not appear. The 3 lines contain the simulation box dimensions for the atom coordinates, in the same format as in a LAMMPS data file (see the [read\\_data](#) command).

The remaining lines each contain an atom ID and its target x,y,z coordinates. The atom lines (all or none of them) can optionally be followed by 3 integer values: nx,ny,nz. For periodic dimensions, they specify which image of the box the atom is considered to be in, i.e. a value of N (positive or negative) means add N times the box length to the coordinate to get the true value.

The atom lines can be listed in any order, but every atom in the group must be listed in the file. Atoms not in the fix group may also be listed; they will be ignored.

TMD statistics are written to file2 every N timesteps, unless N is specified as 0, which means no statistics.

The atoms in the fix tmd group should be integrated (via a fix nve, nvt, npt) along with other atoms in the system.

Restarts can be used with a fix tmd command. For example, imagine a 10000 timestep run with a rho\_initial = 11 and a rho\_final = 1. If a restart file was written after 2000 time steps, then the configuration in the file would have a rho value of 9. A new 8000 time step run could be performed with the same rho\_final = 1 to complete the conformational change at the same transition rate. Note that for restarted runs, the name of the TMD statistics file should be changed to prevent it being overwritten.

For more information about TMD, see [\(Schlitter1\)](#) and [\(Schlitter2\)](#).

### Restrictions:

All TMD fixes must be listed in the input script after all integrator fixes (nve, nvt, npt) are applied. This ensures that atoms are moved before their positions are corrected to comply with the constraint.

Atoms that have a TMD fix applied should not be part of a group to which a SHAKE fix is applied. This is because LAMMPS assumes there are not multiple competing holonomic constraints applied to the same atoms.

**Related commands:** none

**Default:** none

---

**(Schlitter1)** Schlitter, Swegat, Mulders, "Distance-type reaction coordinates for modelling activated processes", J Molecular Modeling, 7, 171–177 (2001).

**(Schlitter2)** Schlitter and Klahn, "The free energy of a reaction coordinate at multiple constraints: a concise formulation", Molecular Physics, 101, 3439–3443 (2003).

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---

## fix uniaxial command

### Syntax:

```
fix ID group-ID uniaxial N keyword dim amount
```

- ID, group-ID are documented in [fix](#) command
- uniaxial = style name of this fix command
- N = perform uniaxial rescaling every this many timesteps
- dim = x or y or z
- strain = uniaxial strain in dim (2.0 = 2x larger)

## Examples:

```
fix 1 all uniaxial 100 x 2.0
```

## Description:

Enable a uniaxial dilation/contraction of the simulation box during a simulation. For example if the direction is X and the strain is 2, then the final box size is  $2L, L/\sqrt{2}, L/\sqrt{2}$ , where  $L^3$  is a cube with the same volume as the initial box, which need not be cubic.

The chosen direction is ramped linearly during the course of the simulation. If the two perpendicular box sizes are equal then the deformation pathway is uniaxial at each timestep. If the two perpendicular box length sizes differ, then their aspect ratio will be linearly ramped down to 1. Irregardless of the initial box shape the total volume is constant during the deformation. Additional details provided by Carsten Svaneborg (Max Planck Institute for Complex Systems, Dresden, Germany) who authored this fix, are at the bottom of this page.

The initial simulation box boundaries at the beginning of a run are specified by the create\_box or read\_data or read\_restart command used to setup the simulation, or they are the values at the end of the previous run. Every Nth timestep during the run, the various dimensions are expanded or contracted. The coordinates of all atoms in the group are also scaled to the new box size.

## Restrictions:

To use this fix, all dimensions of the system must be periodic.

**Related commands:** none

**Default:** none

## Extra Notes:

The uniaxial deformation is performed as follows:

For notational simplicity the deformation is assumed to be in the X direction with final strain  $\lambda$ .  $\alpha$  denotes an arbitrary Cartesian direction.

The initial strain is obtained from box dimensions:

```
lambdai_alpha = Box(alpha)/power(Box(0)*Box(1)*Box(2),1/3)
```

The final strain  $\lambda$  in dir is specified:

```
lambdaf_x = lambda  
lambda_y = lambda_z = 1/sqrt(lambda)
```

Volume conservation implies  $\lambda_x(t)\lambda_y(t)\lambda_z(t) = 1.0$  for all times. Rather than time, let  $\delta$  denote reduced time in the interval from 0 to 1.

We want a linear ramp in the specified strain component, such that MD time steps and uniaxial strain are linearly related:

```
lambda_x(delta) = lambdai_x (1-delta) + lambdaf_x
```

fix uniaxial command

The problem that remains is to choose a deformation pathway for  $\lambda_y(\delta)$  and  $\lambda_z(\delta)$  that agrees with the initial and final strains, and at all times conserves volume. Secondly the pathway should be symmetric if the box has yz symmetry.

In the case where the initial box is symmetric in yz, this follows from volume conservation:

$$\lambda_y(\delta) = \lambda_z(\delta) = 1/\sqrt{\lambda_x(\delta)}$$

However, in general the initial box dimensions in the y and z directions need not be the same so assume a relation:

$$\lambda_y(\delta) = \alpha(\delta)\lambda_z(\delta)$$

From volume conservation it follows that

$$\begin{aligned}\lambda_y(\delta) &= \sqrt{\alpha(\delta)/\lambda_x(\delta)} \\ \lambda_z(\delta) &= 1/\sqrt{\alpha(\delta)*\lambda_x(\delta)}\end{aligned}$$

The asymmetry parameter has to fulfill the following boundary conditions:

$$\begin{aligned}\text{initial } \alpha(\delta=0) &= \lambda_{y0}/\lambda_{z0} \\ \text{final } \alpha(\delta=1) &= 1\end{aligned}$$

Any interpolation that does this will by define a continuous volume conserving deformation from the initial to the desired final state. The freedom of choice here is e.g. to relax the asymmetry of the box very fast, and then slowly elongate along x, or to do this more slowly.

The choice used in the code is:

$$\alpha(\delta) = \lambda_{y0}/\lambda_{z0} (1-\delta) + \delta$$

Note in some cases like strain  $\rightarrow$  strain the perpendicular strains do not follow a monotonic curve.

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---

## fix viscous command

### Syntax:

```
fix ID group-ID viscous gamma keyword values ...
```

- ID, group-ID are documented in [fix](#) command
- viscous = style name of this fix command
- gamma = damping coefficient (force/velocity units)
- zero or more keyword/value pairs can be appended
- keyword = *b* or *a* or *t* or *m*
- zero or more keyword/value pairs may be appended to the args

```
keyword = scale
scale values = type ratio
type = atom type (1-N)
ratio = factor to scale the damping coefficient by
```

### Examples:

```
fix 1 flow viscous 0.1
fix 1 damp viscous 0.5 scale 3 2.5
```

### Description:

Add a viscous damping force to atoms in the group that is proportional to the velocity of the atom. The added force can be thought of as a frictional interaction with implicit solvent. In granular simulations this can be useful for draining the kinetic energy from the system in a controlled fashion. If used without additional thermostating (to add kinetic energy to the system), it has the effect of slowly (or rapidly) freezing the system; hence it is a simple energy minimization technique.

The damping force  $F$  is given by  $F = -\gamma \cdot \text{velocity}$ . The larger the coefficient, the faster the kinetic energy is reduced. If the optional keyword *scale* is used,  $\gamma$  can be scaled up or down by the specified factor for atoms of that type. It can be used multiple times to adjust  $\gamma$  for several atom types.

In a Brownian dynamics context,  $\gamma = kT / mD$ , where  $k$  = Boltzmann's constant,  $T$  = temperature,  $m$  = particle mass, and  $D$  = particle diffusion coefficient.  $D$  can be written as  $kT / (6 \pi \eta d)$ , where  $\eta$  = viscosity of the frictional fluid and  $d$  = diameter of particle. This means  $\gamma = 6 \pi \eta d$ , and thus is proportional to the viscosity of the fluid and the particle diameter.

In the current implementation, rather than have the user specify a viscosity (in centiPoise or some other units),  $\gamma$  is specified directly in force/velocity units. If needed,  $\gamma$  can be adjusted for atoms of different sizes (i.e.  $\sigma$ ) by using the *scale* keyword.

Note that Brownian dynamics models also typically include a randomized force term to thermostat the system at a chosen temperature. The [`fix langevin`](#) command adds both a viscous damping term and this random force to each atom; hence if using `fix langevin` you do not typically need to use `fix viscous`.

**Restrictions:** none

**Related commands:**

[`fix langevin`](#)

**Default:** none

---

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---

## fix volume/rescale command

### Syntax:

```
fix ID group-ID volume/rescale N keyword args ...
```

- ID, group-ID are documented in [`fix`](#) command
- volume/rescale = style name of this fix command
- N = perform volume rescaling every this many timesteps
- one or more keyword/value pairs may be appended to the args

- keyword = *x* or *y* or *z*

*x*, *y*, *z* args = *lo*,*hi* = desired simulation box boundaries  
at end of run (distance units)

### Examples:

```
fix 1 all volume/rescale 100 x -9.0 9.0 z -5.0 5.0
```

### Description:

Enable a volume (density) change during a simulation. Each of the 3 box dimensions is controlled separately. Any dimension being varied by this command must be periodic – see the [boundary](#) command. Dimensions not varied by this command can be periodic or non-periodic. The volume associated with an unspecified dimension can also be controlled by a [fix npt](#) command.

The initial simulation box boundaries at the beginning of a run are specified by the [create\\_box](#) or [read\\_data](#) or [read\\_restart](#) command used to setup the simulation, or they are the values at the end of the previous run. The desired simulation box boundaries at the end of the run are given by the *lo* and *hi* arguments. See the [units](#) command for a discussion of distance units.

Every Nth timestep during the run, the simulation box is expanded or contracted to a ramped value between the initial and final values. The coordinates of all atoms in the group are also scaled to the new box size.

### Restrictions:

Any dimension being varied by this fix must be periodic.

**Related commands:** none

**Default:** none

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---

## fix wall/gran command

### Syntax:

```
fix ID group-ID wall/gran wallstyle args keyword values ...
```

- ID, group-ID are documented in [fix](#) command
- wall/gran = style name of this fix command
- style = *xplane* or *yplane* or *zplane* or *zcylinder*
- args = list of arguments for a particular style

```
xplane or yplane or zplane args = lo hi gamma xmu
  lo, hi = position of lower and upper plane (either can be NULL)
  gamman = damping coeff for normal direction collisions with wall
  xmu = friction coeff for the wall
zcylinder args = radius gamma xmu
  radius = cylinder radius (distance units)
  gamman = damping coeff for normal direction collisions with wall
  xmu = friction coeff for the wall
```

- zero or more keyword/value pairs may be appended to args

```
keyword = wiggle
values = dim amplitude period
dim = x or y or z
amplitude = size of oscillation (distance units)
period = time of oscillation (time units)
```

### Examples:

```
fix 1 all wall/gran xplane -10.0 10.0 50.0 0.5
fix 2 all wall/gran zcylinder 15.0 50.0 0.5 wiggle z 3.0 2.0
fix 1 all wall/gran zplane 0.0 NULL 100.0 0.5
```

### Description:

Bound the simulation domain of a granular system with a frictional wall. All particles in the group interact with the wall when they are close enough to touch it.

The *wallstyle* can be planar or cylindrical. The 3 planar options specify a pair of walls in a dimension. Wall positions are given by *lo* and *hi*. Either of the values can be specified as NULL if a single wall is desired. For a *zcylinder* wallstyle, the cylinder's axis is at  $x = y = 0.0$ , and the radius of the cylinder is specified. For all wallstyles, a damping and friction coefficient for particle–wall interactions are also specified.

Optionally, a wall can be oscillated, similar to the oscillations of frozen particles specified by the [fix\\_wiggle](#) command. This is useful in packing simulations of granular particles. If the keyword *wiggle* is appended to the argument list, then a dimension for the motion, as well as its *amplitude* and *period* is specified. Each timestep, the position of the wall in the appropriate *dim* is set according to this equation:

$$\text{position} = \text{pos0} + A - A \cos(\omega * \text{delta})$$

where *pos0* is the position at the time the fix was specified, *A* is the *amplitude*,  $\omega$  is  $2 \text{ PI} / \text{period}$ , and *delta* is the elapsed time since the fix was specified. The velocity of the wall is also set to the derivative of this expression.

### Restrictions:

Can only be used if LAMMPS was built with the "granular" package. A *zcylinder* wall can only be oscillated in the *z* dimension. This fix can only be used with *atom\_style granular*.

### Related commands:

[fix\\_wiggle](#)

**Default:** none

---

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---

## fix wall/lj93 command

### Syntax:

```
fix ID group-ID wall/lj93 style coord epsilon sigma cutoff
```

- ID, group-ID are documented in [fix](#) command
- wall/lj93 = style name of this fix command
- style = *xlo* or *xhi* or *ylo* or *yhi* or *zlo* or *zhi*
- coord = position of wall
- epsilon = Lennard-Jones epsilon for wall-particle interaction
- sigma = Lennard-Jones sigma for wall-particle interaction
- cutoff = distance from wall at which wall-particle interaction is cut off

### Examples:

```
fix wallhi all wall/lj93 xhi 10.0 1.0 1.0 1.12
```

### Description:

Bound the simulation domain with a Lennard-Jones wall that encloses the atoms. The energy  $E$  of a wall-particle interactions is given by the 9-3 potential

$$E = \epsilon \left[ \frac{2}{15} \left( \frac{\sigma}{r} \right)^9 - \left( \frac{\sigma}{r} \right)^3 \right] \quad r < r_c$$

where  $r$  is the distance from the particle to the wall *coord*, and epsilon and sigma are the usual LJ parameters.  $R_c$  is the cutoff value specified in the command. This interaction is derived by integrating over a 3d half-lattice of Lennard-Jones 12-6 particles.

This fix supports the [fix\\_modify](#) options for *thermo* and *energy*. The former will print the contribution the fix makes to the energy of the system when thermodynamics is printed. The latter will add this contribution to the total potential energy (PotEng).

**Restrictions:** none

**Related commands:**

[fix wall/reflect](#) command

**Default:** none

---

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---



## fix wall/reflect command

### Syntax:

```
fix ID group-ID wall/reflect keyword ...
```

- ID, group-ID are documented in [fix](#) command
- wall/reflect = style name of this fix command
- one or more keyword/value pairs may be appended to the args
- keyword = *xlo* or *xhi* or *ylo* or *yhi* or *zlo* or *zhi*

### Examples:

```
fix xwalls all wall/reflect xlo xhi
fix walls all wall/reflect xlo ylo zlo xhi yhi zhi
```

### Description:

Bound the simulation with one or more walls which reflect particles when they attempt to move thru them. Normally, the simulation domain should be set non-periodic via the [boundary](#) command in any dimension that has such a wall, but LAMMPS does not check for this condition.

Reflection means that if an atom moves outside the box on a timestep by a distance delta (e.g. due to [fix nve](#)), then it is put back inside the box by the same delta and the sign of the corresponding component of its velocity is flipped.

**Restrictions:** none

### Related commands:

[fix wall/lj93](#) command

**Default:** none

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---

## fix wiggle command

### Syntax:

```
fix ID group-ID wiggle dim amplitude period
```

- ID, group-ID are documented in [fix](#) command
- wiggle = style name of this fix command
- dim = *x* or *y* or *z*
- amplitude = size of oscillation (distance units)
- period = time of oscillation (time units)

### Examples:

```
fix 1 frozen wiggle 3.0 0.5
```

fix wall/reflect command

**Description:**

Move a group of atoms in a sinusoidal oscillation. This is useful in granular simulations when boundary atoms are wiggled to induce packing of the dynamic atoms. The dimension *dim* of movement is specified as is the *amplitude* and *period* of the oscillations. Each timestep the *dim* coordinate of each atom is set to

$$\text{coord} = \text{coord0} + A - A \cos(\omega * \text{delta})$$

where *coord0* is the coordinate at the time the fix was specified, *A* is the *amplitude*, *omega* is  $2\pi / \text{period}$ , and *delta* is the elapsed time since the fix was specified. The velocity of the atom is set to the derivative of this expression.

**Restrictions:** none

**Related commands:** none

**Default:** none

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---

## group command

**Syntax:**

```
group ID style args
```

- ID = user-defined name of the group
- style = *region* or *type* or *id* or *molecule* or *subtract* or *union* or *intersect*

```
region args = region-ID
type or id or molecule
  args = one or more atom types, atom IDs, or molecule IDs
  args = logical value
    logical = "<" or ">="
    value = an atom type or atom ID or molecule ID (depending on style)
  args = logical value1 value2
    logical = "<"
    value1,value2 = atom types or atom IDs or molecule IDs
                  (depending on style)
subtract args = two or more group IDs
union args = one or more group IDs
intersect args = two or more group IDs
```

**Examples:**

```
group edge region regstrip
group water type 3 4
group sub id <= 150
group polyA molecule 50 250
group boundary subtract all a2 a3
group boundary union lower upper
group boundary intersect upper flow
```

**Description:**

Identify a collection of atoms as belonging to a group. The group ID can then be used in other commands such as `fix`, `velocity`, `dump`, or `temperature` to act on the atoms together.

If the group ID already exists, the group command adds the specified atoms to the group.

The *region* style puts all atoms in the region volume into the group. Note that this is a static one-time assignment. The atoms remain assigned (or not assigned) to the group even in they later move out of the region volume.

The *type*, *id*, and *molecule* styles put all atoms with the specified atom types, atom IDs, or molecule IDs into the group. These 3 styles can have their arguments specified in one of two formats. The 1st format is a list of values (types or IDs). For example, the 2nd command in the examples above, puts all atoms of type 3 or 4 into the group named *water*. The 2nd format is a *logical* followed by one or two values (type or ID). The 5 valid logicals are listed above. All the logicals except take a single argument. The 3rd example above adds all atoms with IDs from 1 to 150 to the group named *sub*. The logical means "between" and takes 2 arguments. The 4th example above adds all atoms belonging to molecules with IDs from 50 to 250 (inclusive) to the group named *polyA*.

The *subtract* style takes a list of two or more existing group names as arguments. All atoms that belong to the 1st group, but not to any of the other groups are added to the specified group.

The *union* style takes a list of one or more existing group names as arguments. All atoms that belong to any of the listed groups are added to the specified group.

The *intersect* style takes a list of two or more existing group names as arguments. Atoms that belong to every one of the listed groups are added to the specified group.

A group with the ID *all* is predefined. All atoms belong to this group.

#### **Restrictions:**

There can be no more than 32 defined groups, including "all".

#### **Related commands:**

`region`, `fix`, `velocity`, `dump`, `temperature`

#### **Default:**

All atoms belong to the "all" group.

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---

## **improper\_coeff command**

### **Syntax:**

```
improper_coeff N args
```

- N = improper type (see asterik form below)

- args = coefficients for one or more improper types

### Examples:

```
improper_coeff 1 300.0 0.0
improper_coeff * 80.2 -1 2
improper_coeff *4 80.2 -1 2
```

### Description:

Specify the force field coefficients for one or more improper types. The number and meaning of the coefficients depends on the improper style. As described below, improper coefficients can also be set in the data file read by the [read\\_data](#) command or in a restart file.

N can be specified in one of two ways. An explicit numeric value can be used, as in the 1st example above. Or a wild-card asterik can be used to set the coefficients for multiple improper types. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If N = the number of improper types, then an asterik with no numeric values means all types from 1 to N. A leading asterik means all types from 1 to n (inclusive). A trailing asterik means all types from n to N (inclusive). A middle asterik means all types from m to n (inclusive).

Note that using 2 improper\_coeff commands for the same improper type is perfectly valid. For example, these commands set the coeffs for all improper types, then overwrite the coeffs for just improper type 2:

```
improper_coeff * 300.0 0.0
improper_coeff 2 50.0 0.0
```

A line in a data file that specifies improper coefficients uses the exact same format as the arguments of the improper\_coeff command in an input script, except that wild-card asteriks should not be used since coefficients for all N types are listed in the file. For example, under the "Improper Coeffs" section of a data file, the line that corresponds to the 1st example above would be listed as

```
1 300.0 0.0
```

See the [improper\\_style](#) command for more discussion of the formulas that use these coefficients. The [units](#) of each coefficient are shown in parenthesis.

$$\begin{aligned}
 E &= E_i + E_{aa} \\
 E_i &= K \left[ \frac{\chi_{ijkl} + \chi_{kjli} + \chi_{ljik}}{3} - \chi_0 \right]^2 \\
 E_{aa} &= M_1(\theta_{ijk} - \theta_1)(\theta_{kjl} - \theta_3) + \\
 &\quad M_2(\theta_{ijk} - \theta_1)(\theta_{ijl} - \theta_2) + \\
 &\quad M_3(\theta_{ijl} - \theta_2)(\theta_{kjl} - \theta_3)
 \end{aligned}$$

For style *class2*, only coefficients for the  $E_i$  formula can be specified in the input script. These are the 2 coefficients:

- K (energy/radian^2)
- X0 (degrees)

X0 is specified in degrees, but LAMMPS converts it to radians internally; hence the units of K are in energy/radian^2.

Coefficients for the Eaa formula must be specified in the data file. For the Eaa formula, the coefficients are listed under a "AngleAngle Coeffs" heading and each line lists 6 coefficients:

- M1 (energy/distance)
- M2 (energy/distance)
- M3 (energy/distance)
- theta1 (degrees)
- theta2 (degrees)
- theta3 (degrees)

The theta values are specified in degrees, but LAMMPS converts them to radians internally; hence the units of M are in energy/radian^2.

---

$$E = K[1 + d \cos(n\phi)]$$

For style *cvff*, specify 3 coefficients:

- K (energy)
  - d (+1 or -1)
  - n (0,1,2,3,4,6)
- 

$$E = K(\chi - \chi_0)^2$$

For style *harmonic*, specify 2 coefficients:

- K (energy/radian^2)
- X0 (degrees)

X0 is specified in degrees, but LAMMPS converts it to radians internally; hence the units of K are in energy/radian^2.

---

For style *hybrid*, the first coefficient sets the improper style and the remaining coefficients are those appropriate to that style. For example, these commands:

```
improper_coeff 1 cvff 20.0 -1 2
improper_coeff 2 harmonic 120.0 30
```

would set bonds of improper type 1 to be computed with a *cvff* potential. Likewise, impropers of improper type 2 would be computed with a *harmonic* potential.

---

### Restrictions:

This command must come after the simulation box is defined by a read\_data, read\_restart, or create\_box command.

An improper style must be defined before any improper coefficients are set, either in the input script or in a data file.

#### Related commands:

[improper\\_style](#)

**Default:** none

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---

## improper\_style command

### Syntax:

```
improper_style style
```

- style = *none* or *class2* or *cvff* or *harmonic* or *hybrid*

### Examples:

```
improper_style harmonic
improper_style cvff
improper_style hybrid cvff harmonic
```

### Description:

Set the formula(s) LAMMPS will use to compute improper interactions between quadruplets (trigonal centers) of atoms. The list of atom quadruplets is specified in the data or restart file and is read in by a [read\\_data](#) or [read\\_restart](#) command. The coefficients for the formula for each improper type can also be specified in those files or by the [improper\\_coeff](#) command.

A style of *none* means improper forces are not computed, even if impropers are defined.

---

The *class2* style uses the potential

$$\begin{aligned}
 E &= E_i + E_{aa} \\
 E_i &= K \left[ \frac{\chi_{ijkl} + \chi_{kjli} + \chi_{ljik}}{3} - \chi_0 \right]^2 \\
 E_{aa} &= M_1(\theta_{ijk} - \theta_1)(\theta_{kjl} - \theta_3) + \\
 &\quad M_2(\theta_{ijk} - \theta_1)(\theta_{ijl} - \theta_2) + \\
 &\quad M_3(\theta_{ijl} - \theta_2)(\theta_{kjl} - \theta_3)
 \end{aligned}$$

where  $E_i$  is the improper term and  $E_{aa}$  is an angle–angle term. The  $\chi$  used in  $E_i$  is an average over 3 possible  $\chi$  orientations. The subscripts on the various  $\theta$ 's refer to different combinations of atoms  $i, j, k, l$  used to form the angle;  $\theta_1, \theta_2, \theta_3$  are the equilibrium positions of those angles.  $K, M_1, M_2, M_3, \chi_0$  are coefficients defined for each improper type.

---

The *cvff* style uses the potential

improper\_style command

$$E = K[1 + d \cos(n\phi)]$$

where  $\phi$  is the Wilson out-of-plane angle. K, d, and n are coefficients defined for each improper type.

---

The *harmonic* style uses the potential

$$E = K(\chi - \chi_0)^2$$

where  $\chi$  is the improper angle,  $\chi_0$  is its equilibrium value, and K is a prefactor. Note that the usual 1/2 factor is included in K. K and  $\chi_0$  are coefficients defined for each improper type.

---

The *hybrid* style enables the use of multiple improper styles in one simulation. An improper style is assigned to each improper type. For example, impropers in a polymer flow (of improper type 1) could be computed with a *cvff* potential and impropers in the wall boundary (of improper type 2) could be computed with a *harmonic* potential. The assignment of improper type to style is made via the `improper_coeff` command or in the data file.

---

### Restrictions:

Improper styles can only be set for atom\_style choices that allow impropers to be defined.

Improper styles are part of the "molecular" package. They are only enabled if LAMMPS was built with that package. See the [Making LAMMPS](#) section for more info.

### Related commands:

[`improper\_coeff`](#)

### Default:

```
improper_style none
```

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---

## include command

### Syntax:

```
include file
```

- file = filename of new input script to switch to

### Examples:

```
include newfile
include in.run2
```

**Description:**

This command opens a new input script file and begins reading LAMMPS commands from that file. When the new file is finished, the original file is returned to. Include files can be nested as deeply as desired. If input script A includes script B, and B includes A, then LAMMPS could run for a long time.

If the filename is a variable (see the [variable](#) command), different processor partitions can run different input scripts.

**Restrictions:** none

**Related commands:**

[variable](#), [jump](#)

**Default:** none

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---

## jump command

**Syntax:**

```
jump file label
```

- file = filename of new input script to switch to
- label = optional label within file to jump to

**Examples:**

```
jump newfile  
jump in.run2 runloop
```

**Description:**

This command closes the current input script file, opens the file with the specified name, and begins reading LAMMPS commands from that file. The original file is not returned to, although by using multiple jump commands it is possible to chain from file to file or back to the original file.

Optionally, if a 2nd argument is used, it is treated as a label and the new file is scanned (without executing commands) until the label is found, and commands are executed from that point forward. This can be used to loop over a portion of the input script, as in this example. These commands perform 10 runs, each of 10000 steps, and create 10 dump files named file.1, file.2, etc. The [next](#) command is used to exit the loop after 10 iterations. When the "a" variable has been incremented for the 10th time, it will cause the next jump command to be skipped.

```
variable a loop 10  
label loop  
dump 1 all atom 100 file.$a  
run 10000  
undump 1  
next a
```



```
jump in.lj loop
```

If the *jump file* argument is a variable, the jump command can be used to cause different processor partitions to run different input scripts. In this example, LAMMPS is run on 40 processors, with 4 partitions of 10 procs each. An in.file containing the example variable and jump command will cause each partition to run a different simulation.

```
mpirun -np 40 lmp_ibm -partition 4x10 -in in.file
```

```
variable f world script.1 script.2 script.3 script.4
jump $f
```

### Restrictions:

If you jump to a file and it does not contain the specified label, LAMMPS will come to the end of the file and exit.

### Related commands:

[variable](#), [include](#), [label](#), [next](#)

**Default:** none

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---

## kspace\_modify command

### Syntax:

```
kspace_modify keyword value ...
```

- one or more keyword/value pairs may be listed
- keyword = *mesh* or *order* or *gewald* or *slab*

```
mesh value = x y z
  x,y,z = PPPM FFT grid size in each dimension
order value = N
  N = grid extent of Gaussian for PPPM mapping of each charge
gewald value = r
  r = PPPM G-ewald parameter
slab value = volfactor
  volfactor = ratio of the total extended volume used in the
              2d approximation compared with the volume of the simulation domain
```

### Examples:

```
kspace_modify mesh 24 24 30 order 6
kspace_modify slab 3.0
```

### Description:

Set parameters used by the kspace solvers defined by the [kspace\\_style](#) command. Not all parameters are relevant to all kspace styles.

The *mesh* keyword sets the 3d FFT grid size for kspace style ppm. Each dimension must be factorizable into powers of 2, 3, and 5. When this option is not set, the PPPM solver chooses its own grid size, consistent with the user-specified accuracy and pairwise cutoff. Values for x,y,z of 0,0,0 unset the option.

The *order* keyword determines how many grid spacings an atom's charge extends when it is mapped to the FFT grid in kspace style ppm. The default for this parameter is 5, which means each charge spans 5 grid cells in each dimension.

The *gewald* keyword sets the value of the PPPM G-ewald parameter. Without this setting, LAMMPS chooses the parameter automatically as a function of cutoff, precision, grid spacing, etc. This means it can vary from one simulation to the next which may not be desirable for matching a KSpace solver to a pre-tabulated pairwise potential. This setting can also be useful if PPPM fails to choose a good grid spacing and G-ewald parameter automatically. If the value is set to 0.0, LAMMPS will choose the G-ewald parameter automatically.

The *slab* keyword allows an Ewald or PPPM solver to be used for a systems that are periodic in x,y but non-periodic in z – a boundary setting of "boundary p p f". This is done by treating the system as if it were periodic in z, but inserting empty volume between atom slabs and removing dipole inter-slab interactions so that slab-slab interactions are effectively turned off. The volfactor value sets the ratio of the extended dimension in z divided by the actual dimension in z. The recommended value is 3.0. A larger value is inefficient; a smaller value introduces unwanted slab-slab interactions. The use of fixed boundaries in z means that the user must prevent particle migration beyond the initial z-bounds, typically by providing a wall-style fix.

**Restrictions:** none

**Related commands:**

kspace\_style, boundary

**Default:**

The option defaults are mesh = 0 0 0, order = 5, gewald = 0.0, and slab = 1.0.

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---

## kspace\_style command

**Syntax:**

kspace\_style style value

- style = *none* or *ewald* or *pppm*

```
none value = none
ewald value = precision
precision = desired accuracy
pppm value = precision
precision = desired accuracy
pppm/tip4p value = precision
precision = desired accuracy
```

## Examples:

```
kspace_style ppm 1.0e-4  
kspace_style none
```

## Description:

Define a K-space solver for LAMMPS to use each timestep to compute long-range Coulombic interactions. When such a solver is used in conjunction with an appropriate pair style, the cutoff for Coulombic interactions is effectively infinite; each charge in the system interacts with charges in an infinite array of periodic images of the simulation domain.

The *ewald* style performs a standard Ewald summation as described in any solid-state physics text.

The *pppm* style invokes a particle-particle particle-mesh solver ([Hockney](#)) which maps atom charge to a 3d mesh, uses 3d FFTs to solve Poisson's equation on the mesh, then interpolates electric fields on the mesh points back to the atoms. It is closely related to the particle-mesh Ewald technique (PME) ([Darden](#)) used in AMBER and CHARMM. The cost of traditional Ewald summation scales as  $N^{3/2}$  where  $N$  is the number of atoms in the system. The PPPM solver scales as  $N \log(N)$  due to the FFTs, so it is almost always a faster choice ([Pollock](#)).

The *pppm/tip4p* style is identical to the *pppm* style except that it adds a charge at the massless 4th site in each TIP4P water molecule. It should be used with [pair styles](#) with a *long/tip4p* in their style name.

When a kspace style is used, a pair style that includes the short-range correction to the pairwise Coulombic forces must also be selected. These styles are ones that have a *coul/long* in their style name.

A precision value of 1.0e-4 means one part in 10000. This setting is used in conjunction with the pairwise cutoff to determine the number of K-space vectors for style *ewald* or the FFT grid size for style *pppm*.

## Restrictions:

A simulation must be 3d and periodic in all dimensions to use an Ewald or PPPM solver. The only exception is if the slab option is set with [kspace\\_modify](#), in which case the xy dimensions must be periodic and the z dimension must be non-periodic.

Kspace styles are part of the "kspace" package. They are only enabled if LAMMPS was built with that package. See the [Making LAMMPS](#) section for more info.

When using a long-range pairwise TIP4P potential, you must use kspace style *pppm/tip4p* and vice versa.

## Related commands:

[kspace\\_modify](#), [pair\\_style lj/cut/coul/long](#), [pair\\_style lj/charmm/coul/long](#)

## Default:

```
kspace_style none
```

---

(**Darden**) Darden, York, Pedersen, J Chem Phys, 98, 10089 (1993).

(Hockney) Hockney and Eastwood, Computer Simulation Using Particles, Adam Hilger, NY (1989).

(Pollock) Pollock and Glosli, Comp Phys Comm, 95, 93 (1996).

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## label command

### Syntax:

```
label ID
```

- ID = string used as label name

### Examples:

```
label xyz
label loop
```

### Description:

Label this line of the input script with the chosen ID. Unless a `jump` command was used previously, this does nothing. But if a `jump` command was used with a label argument to begin invoking this script file, then all command lines in the script prior to this line will be ignored. I.e. execution of the script will begin at this line. This is useful for looping over a section of the input script as discussed in the `jump` command.

**Restrictions:** none

**Related commands:** none

**Default:** none

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---

## lattice command

### Syntax:

```
lattice style value
```

- style = *none* or *sc* or *bcc* or *fcc* or *sq* or *sq2* or *hex*

```
none value = none
```

```
for all other styles:
```

```
value = reduced density (for LJ units)
```

```
value = cubic lattice constant in Angstroms (for real or metal units)
```

### Examples:

```
lattice fcc 3.52
lattice hex 0.85
```

lattice none

### Description:

Define a lattice type and lattice constant. This is required before using a commands that (optionally) use the lattice, such as [create\\_atoms](#) or [region](#). The lattice type must be consistent with the dimension of the simulation – see the [dimension](#) command. Styles *sc* or *bcc* or *fcc* are for 3d problems. Styles *sq* or *sq2* or *hex* are for 2d problems. Lattices of style *fcc*, *bcc*, *sc*, or *hex* are described in any solid–state physics text. A *sq* lattice is one with atoms at the corners of a square. A *sq2* lattice is a *sq* lattice with an additional atom at the center of the square.

For unit style *real* or *metal*, the specified value is the cubic lattice constant in Angstroms. For unit style *lj*, the value is the reduced density ( $\rho^*$ ) which LAMMPS converts into a cubic lattice constant. For 3d problems, the relationship " $\rho^* = \rho \sigma^3$ " is used for the conversion, where  $\rho = N/V$  with  $V$  = the volume of the cubic cell and  $N = 4$  for *fcc*, 2 for *bcc*, and 1 for *sc* (simple cubic) lattices. For 2d problems, the relationship " $\rho^* = \rho \sigma^2$ " is used for the conversion, where  $N = 2$  for *sq2* or *hex* and 1 for *sq*. In the hex case, the unit cell is actually rectangular; it is extended by a factor of  $\sqrt{3}$  in the  $y$ -dimension.

The command "lattice none" can be used to turn off the lattice setting. Any command that attempts to use a lattice constant will then generate an error.

**Restrictions:** none

### Related commands:

[dimension](#), [orient](#), [origin](#), [create\\_atoms](#), [region](#)

### Default:

lattice none

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## log command

### Syntax:

log file

- file = name of new logfile

### Examples:

log log.equil

### Description:

This command closes the current LAMMPS log file, opens a new file with the specified name, and begins logging information to it. If the specified file name is *none*, then no new log file is opened.

If multiple processor partitions are being used, the file name should be a variable, so that different processors do not attempt to write to the same log file.

The file "log.lammps" is the default log file for a LAMMPS run. The name of the initial log file can also be set by the command-line switch `-log`. See [this section](#) for details.

**Restrictions:** none

**Related commands:** none

**Default:**

The default LAMMPS log file is named log.lammps

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---

## mass command

**Syntax:**

```
mass I value
```

- I = atom type (see asterik form below)
- value = mass

**Examples:**

```
mass 1 1.0
mass * 62.5
mass 2* 62.5
```

**Description:**

Set the mass for all atoms of one or more atom types. Mass values can also be set in the [read\\_data](#) data file. See the [units](#) command for what mass units to use.

I can be specified in one of two ways. An explicit numeric value can be used, as in the 1st example above. Or a wild-card asterik can be used to set the mass for multiple atom types. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If N = the number of atom types, then an asterik with no numeric values means all types from 1 to N. A leading asterik means all types from 1 to n (inclusive). A trailing asterik means all types from n to N (inclusive). A middle asterik means all types from m to n (inclusive).

A line in a data file that specifies mass uses the exact same format as the arguments of the mass command in an input script, except that no wild-card asterik can be used. For example, under the "Masses" section of a data file, the line that corresponds to the 1st example above would be listed as

```
1 1.0
```

**Restrictions:**

This command must come after the simulation box is defined by a [read\\_data](#), [read\\_restart](#), or [create\\_box](#)

command.

All masses must be defined before a simulation is run (if the atom style requires masses be set). They must also all be defined before a velocity or fix shake command is used.

Masses are not set for atom style granular. This is because each atom is assigned an individual mass in the data or restart file.

**Related commands:** none

**Default:** none

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## min\_modify command

### Syntax:

min\_modify keyword values ...

- one or more keyword/value pairs may be listed

```
keyword = linestyle or dmin or dmax or lineiter
linestyle value = secant or scan
dmin value = min
    min = minimum distance for line search to move (distance units)
dmax value = max
    max = maximum distance for line search to move (distance units)
lineiter value = N
    N = max number of iterations in a line search
```

### Examples:

```
min_modify linestyle scan dmin 0.001 dmax 0.2
min_modify lineiter 5
```

### Description:

This command sets parameters that affect the minimization algorithms. The various settings may effect the convergence rate and overall number of force evaluations required by a minimization, so users can experiment with these parameters to tune their minimizations.

The *linestyle* sets the algorithm used for 1d line searches at each outer iteration of the minimizer. The *secant* style uses two successive force/energy evaluations to create a parabola and pick its minimum as an estimate of the next iteration's 1d minimum. The *scan* style starts its 1d search at *dmin* and doubles the distance along the line at which the energy is computed until the minimum is passed. It continues only as far as *dmax*. Normally, the *secant* method should find more accurate 1d minimums in less iterations, but the *scan* method can be more robust.

The *dmin* and *dmax* settings are both used by the *scan* line search as described above. For the *secant* line search, only the *dmin* value is used to pick an initial point to begin the secant approximation.

The *lineiter* setting is used by the *secant* algorithm to limit its iterations. The smaller the setting, the more inaccurate the line search becomes. Nonlinear conjugate gradient is not thought to require high-accuracy line searches in order to converge efficiently.

**Restrictions:** none

**Related commands:**

[min\\_style](#), [minimize](#)

**Default:**

The option defaults are `linestyle = secant`, `dmin = 1.0e-5`, `dmax = 0.1`, and `lineiter = 10`.

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---

## min\_style command

**Syntax:**

```
min_style style
```

- `style = cg` or `cg/fr` or `sd`

**Examples:**

```
min_style cg
min_style sd
```

**Description:**

Choose a minimization algorithm to use when a [minimize](#) command is performed.

Style *cg* is the Polak–Ribiere (PR) version of the conjugate gradient (CG) algorithm. At each iteration the force gradient is combined with the previous iteration information to compute a new search direction perpendicular (conjugate) to previous search directions. The PR variant affects how the direction is chosen and how the CG method is restarted when it ceases to make progress. The PR variant is thought to be the most effective CG choice.

Style *cg/fr* is the Fletcher–Reeves version of the conjugate gradient algorithm.

Style *sd* is a steepest descent algorithm. At each iteration, the downhill direction corresponding to the force vector (negative gradient of energy) is searched along by a 1d line search. Typically, steepest descent will not converge as quickly as CG, but may be more robust in some situations.

**Restrictions:** none

**Related commands:**

[min\\_modify](#), [minimize](#)



**Default:**

```
min_style cg
```

## minimize command

**Syntax:**

```
minimize tolerance maxiter maxeval
```

- tolerance = stopping tolerance
- maxiter = max iterations of minimizer
- maxeval = max number of total force/energy evaluations

**Examples:**

```
minimize 1.0e-4 100 1000
```

**Description:**

Perform an energy minimization of the system, by adjusting each atom's atomic coordinates. The algorithm used is set by the min\_style command. Minimize commands can be interspersed with run commands to alternate between relaxation and dynamics. The minimizers are implemented in a robust fashion that should allow for systems with highly overlapped atoms (large energies and forces) to still be minimized by pushing the atoms off of each other.

A minimization involves an outer iteration loop which sets the search direction along which coordinates are changed. An inner iteration is then performed using a line search algorithm. The line search typically evaluates forces and energies several times to set new coordinates. The minimization stops if any of several criteria are met:

- the change in energy between outer iterations is less than the tolerance
- the number of outer iterations exceeds maxiter
- the number of force evaluations exceeds maxeval
- the 3N dimensional force vector goes (nearly) to zero

For the first criterion, the specified tolerance is unitless; it is met when the ratio of the energy delta to the energy magnitude is equal to the tolerance (e.g. one part in  $1.0\text{e-}4$ ).

During a minimization, the outer iteration count is treated as a timestep. Output is triggered by this timestep, e.g. thermodynamic output or dump and restart files.

For optimal convergence, a pair\_style that goes smoothly to 0.0 at the cutoff distance for both energy and force should typically be used though this is not required. Examples include *pair/lj/charmm/coul/charmm* and *pair/lj/charmm/coul/long*. If a *soft* potential is used the Astop value is used for the prefactor (no time dependence).

Only fixes that apply force constraints are invoked during minimization. The list of the currently implemented ones include *fix addforce*, *aveforce*, *enforce2d*, *indent*, *lineforce*, *plane force*, *setforce*, and *wall/lj93*.

Following the minimization a statistical summary is printed that includes the energy change and convergence criteria information.

### Restrictions:

Two features that are not yet implemented listed here, in case someone knows how they could be coded:

Two fixes not invoked by a minimization are fix shake and fix rigid. The effect of a fix shake can be approximated during a minimization by using stiff spring constants for the bonds and/or angles that would normally be constrained by the SHAKE algorithm.

The volume of the simulation domain is not allowed to change during a minimization. Ideally we would allow a fix such as *npt* to impose an external pressure that would be included in the minimization (i.e. allow the box dimensions to change), but this has not yet been implemented.

### Related commands:

min\_modify, min\_style, run\_style

**Default:** none

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---

## neigh\_modify command

### Syntax:

```
neigh_modify keyword values ...
```

- one or more keyword/value pairs may be listed

```
keyword = delay or every or check or exclude or page or one
delay value = N
    N = delay building until this many steps since last build
every value = M
    M = build neighbor list every this many steps
check value = yes or no
    yes = only build if some atom has moved half the skin distance or more
    no = always build on 1st step that every and delay are satisfied
exclude values:
    type M N
        M,N = exclude if one atom in pair is type M, other is type N
    group group1-ID group2-ID
        group1-ID,group2-ID = exclude if one atom is in 1st group, other in 2nd
    molecule group-ID
        groupname = exclude if both atoms are in the same molecule and in the same group
    none
        delete all exclude settings
page value = N
    N = number of pairs stored in a single neighbor page
one value = N
    N = max number of neighbors of one atom
```

### Examples:

neigh\_modify command

```
neigh_modify every 2 delay 10 check yes page 100000
neigh_modify exclude type 2 3
neigh_modify exclude group frozen frozen check no
neigh_modify exclude group residue1 chain3
neigh_modify exclude molecule rigid
```

## Description:

This command sets parameters that affect the pairwise neighbor list.

The *every*, *delay*, and *check* options affect how often the list is built as a simulation runs. The *delay* setting means never build a new list until at least N steps after the previous build. The *every* setting means build the list every M steps (after the delay has passed). If the *check* setting is *no*, the list is built on the 1st step that satisfies the *delay* and *every* settings. If the *check* setting is *yes*, then the list is only built on a particular step if some atom has moved more than half the skin distance (specified in the neighbor command) since the last build.

When the rRESPA integrator is used (see the run\_style command), the *every* and *delay* parameters refer to the longest (outermost) timestep.

The *exclude* option turns off pairwise interactions between certain pairs of atoms, by not including them in the neighbor list. These are sample scenarios where this is useful:

- In crack simulations, pairwise interactions can be shut off between 2 slabs of atoms to effectively create a crack.
- When a large collection of atoms is treated as frozen, interactions between those atoms can be turned off to save needless computation. E.g. Using the fix setforce command to freeze a wall or portion of a bio-molecule.
- When one or more rigid bodies are specified, interactions within each body can be turned off to save needless computation. See the fix rigid command for more details.

The *exclude type* option turns off the pairwise interaction if one atom is of type M and the other of type N. M can equal N. The *exclude group* option turns off the interaction if one atom is in the first group and the other is the second. Group1-ID can equal group2-ID. The *exclude molecule* option turns off the interaction if both atoms are in the specified group and in the same molecule, as determined by their molecule ID.

Each of the exclude options can be specified multiple times. The *exclude type* option is the most efficient option to use; it requires only a single check, no matter how many times it has been specified. The other exclude options are more expensive if specified multiple times; they require one check for each time they have been specified.

Note that the exclude options only affect pairwise interactions; see the delete\_bonds command for information on turning off bond interactions.

The *page* and *one* options affect how memory is allocated for the neighbor lists. For most simulations the default settings for these options are fine, but if a very large problem is being run or a very long cutoff is being used, these parameters can be tuned. The indices of neighboring atoms are stored in "pages", which are allocated one after another as they fill up. The size of each page is set by the *page* value. A new page is allocated when the next atom's neighbors could potentially overflow the list. This threshold is set by the *one* value which tells LAMMPS the maximum number of neighbor's one atom can have.

## Restrictions:

neigh\_modify command

If the "delay" setting is non-zero, then it must be a multiple of the "every" setting.

The exclude molecule option can only be used with atom styles that define molecule IDs.

**Related commands:**

[neighbor](#), [delete\\_bonds](#)

**Default:**

The option defaults are delay = 10, every = 1, check = yes, exclude = none, page = 10000, and one = 2000.

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## neighbor command

**Syntax:**

```
neighbor skin style
```

- skin = extra distance beyond force cutoff (distance units)
- style = *bin* or *nsq*

**Examples:**

```
neighbor 0.3 bin  
neighbor 2.0 nsq
```

**Description:**

This command sets parameters that affect the building of the pairwise neighbor list. All atom pairs within a cutoff distance equal to the their force cutoff plus the *skin* distance are stored in the list. Typically, the larger the skin distance, the less often neighbor lists need to be built, but more pairs must be checked for possible force interactions every timestep.

The *style* value chooses what algorithm is used to build the list. *Binning* is an operation that scales linearly with N, the number of atoms on a processor. It is almost always faster than the *nsq* style which scales as N<sup>2</sup>. For unsolvated small molecules in a non-periodic box, the *nsq* choice can sometimes be faster. Either style should give the same answers.

The default values for *skin* and *style* depend on the choice of units for the simulation.

The [neigh\\_modify](#) command has additional options that control how often neighbor lists are built and which pairs are stored in the list.

When a run is finished, counts of the number of neighbors stored in the pairwise list and the number of times neighbor lists were built are printed to the screen and log file. See [this section](#) for details.

**Restrictions:** none

**Related commands:**

neighbor command

neigh\_modify, units

**Default:**

0.3 bin            for lj units  
2.0 bin            for real or metal units

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---

## newton command

**Syntax:**

```
newton flag  
newton flag1 flag2
```

- flag = *on* or *off* for both pairwise and bonded interactions
- flag1 = *on* or *off* for pairwise interactions
- flag2 = *on* or *off* for bonded interactions

**Examples:**

```
newton off  
newton on off
```

**Description:**

This command turns Newton's 3rd law *on* or *off* for pairwise and bonded interactions. For most problems, setting Newton's 3rd law to *on* means a modest savings in computation at the cost of two times more communication. Whether this is faster depends on problem size, force cutoff lengths, a machine's compute/communication ratio, and how many processors are being used.

Setting the pairwise newton flag to *off* means that if two interacting atoms are on different processors, both processors compute their interaction and the resulting force information is not communicated. Similarly, for bonded interactions, newton *off* means that if a bond, angle, dihedral, or improper interaction contains atoms on 2 or more processors, the interaction is computed by each processor.

LAMMPS should produce the same answers for any newton flag settings, except for round-off issues.

With run\_style respa and only bonded interactions (bond, angle, etc) computed in the innermost timestep, it may be faster to turn newton *off* for bonded interactions, to avoid extra communication in the innermost loop.

**Restrictions:**

The newton bond setting cannot be changed after the simulation box is defined by a read\_data or create\_box command.

**Related commands:**

run\_style respa

## Default:

newton on

## next command

### Syntax:

```
next variables
```

- variables = one or more lower-case single-character variable names

### Examples:

```
next x
next a t x
```

### Description:

This command is used with variables defined by the [variable](#) command. It assigns the next value to the variable from the variable's list, so that when \$X is subsequently substituted for in an input script command, the new value is used. X is a single lower-case character from "a" to "z".

All variables in a single next command must be the same style: *index*, *loop*, or *universe*. *Equal*– or *world*–style variables cannot be incremented by a next command.

When any of the variables in the next command has no more values, a flag is set that causes the input script to skip the next [jump](#) command encountered. This enables a loop containing a next command to exit.

When the next command is used with *index*– or *loop*–style variables, the next value is assigned to the variable for all processors. When the next command is used with *universe*–style variables, the next value is assigned to whichever processor partition executes the command first. All processors in the partition are assigned the same value. Running LAMMPS on multiple partitions of processors via the "–partition" command–line switch is described in [this section](#) of the manual. *Universe*–style variables are incremented using the files "tmp.lammps.variable" and "tmp.lammps.variable.lock" which you will see in your directory during such a LAMMPS run.

Here is an example of running a series of simulations using the next command with an *index*–style variable. If this input script is named in.polymer, 8 simulations would be run using data files from directories run1 thru run8.

```
variable d index run1 run2 run3 run4 run5 run6 run7 run8
cd $d
read_data data.polymer
run 10000
cd ..
clear
next d
jump in.polymer
```

If the variable "d" were of style *universe*, and the same in.polymer input script were run on 3 partitions of processors, then the first 3 simulations would begin, one on each set of processors. Whichever partition finished first, it would assign variable "d" the 4th value and run another simulation, and so forth until all 8 simulations were finished.

Jump and next commands can also be nested to enable multi-level loops. For example, this script will run 15 simulations in a double loop.

```
variable i loop 3 variable j loop 5 clear ... read_data data.polymer.$i$j print Running simulation $i.$j run 10000 next j jump in.script next i jump in.script
```

**Restrictions:** none

**Related commands:**

[variable](#), [jump](#), [include](#)

**Default:** none

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---

## orient command

**Syntax:**

```
orient dim i j k
```

- dim = *x* or *y* or *z*
- i,j,k = orientation of lattice that is along box direction dim

**Examples:**

```
orient x 1 1 0
orient y -1 1 0
orient z 0 0 1
```

**Description:**

Specify the orientation of a cubic lattice along simulation box directions *x* or *y* or *z*. These 3 basis vectors are used when the [create\\_atoms](#) command generates a lattice of atoms.

The 3 basis vectors B1, B2, B3 must be mutually orthogonal and form a right-handed system such that B1 cross B2 is in the direction of B3.

The basis vectors should be specified in an irreducible form (smallest possible integers), though LAMMPS does not check for this.

**Restrictions:** none

**Related commands:**

orient command

origin, create\_atoms

**Default:**

```
orient x 1 0 0
orient y 0 1 0
orient z 0 0 1
```

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---

## origin command

**Syntax:**

```
origin x y z
```

- x,y,z = origin of a lattice

**Examples:**

```
origin 0.0 0.5 0.5
```

**Description:**

Set the origin of the lattice defined by the lattice command. The lattice is used by the create\_atoms command to create new atoms and by other commands that use a lattice spacing as a distance measure. This command offsets the origin of the lattice from the (0,0,0) coordinate of the simulation box by some fraction of a lattice spacing in each dimension.

The specified values are in lattice coordinates from 0.0 to 1.0, so that a value of 0.5 means the lattice is displaced 1/2 a cubic cell.

**Restrictions:** none

Related commands:

lattice, orient

**Default:**

```
origin 0 0 0
```

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---

## pair\_coeff command

**Syntax:**

```
pair_coeff I J args
```

- I,J = atom types (see asterik form below)



- args = coefficients for one or more pairs of atom types

### Examples:

```
pair_coeff 2 2 1.0 1.0 2.5
pair_coeff 2 * 1.0 1.0
pair_coeff 3* 1*2 1.0 1.0 2.5
pair_coeff * * 1.0 1.0
pair_coeff 2 2 niu3
pair_coeff * * nialhjea 1 1 2
pair_coeff * 3 morse.table ENTRY1
pair_coeff 1 2 lj/cut 1.0 1.0 2.5
```

### Description:

Specify the pairwise force field coefficients for one or more pairs of atom types. The number and meaning of the coefficients depends on the pair style. Pair coefficients can also be set in the data file read read\_data command or in a restart file.

I and J can be specified in one of two ways. Explicit numeric values can be used for each, as in the 1st example above. In this case,  $I \leq J$  is required. LAMMPS sets the coefficients for the symmetric J,I interaction to the same values.

A wild-card asterik can be used with the I,J arguments to set the coefficients for multiple pairs of atom types. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If N = the number of atom types, then an asterik with no numeric values means all types from 1 to N. A leading asterik means all types from 1 to n (inclusive). A trailing asterik means all types from n to N (inclusive). A middle asterik means all types from m to n (inclusive). Note that only type pairs with  $I \leq J$  are set; if asteriks imply type pairs where  $J < I$ , they are ignored.

Note that using 2 pair\_coeff commands for the same I,J pair is perfectly valid. For example, these commands set the coeffs for all I,J pairs, then overwrite the coeffs for just the I,J = 2,3 pair:

```
pair_coeff * * 1.0 1.0 2.5
pair_coeff 2 3 2.0 1.0 1.12
```

A line in a data file that specifies pair coefficients uses the exact same format as the arguments of the pair\_coeff command in an input script, with the exception of the I,J type arguments. In each line of the "Pair Coeffs" section of a data file, only a single type I is specified, which sets the coefficients for type I interacting with type I. This is because the section has exactly N lines, where N = the number of atom types. For this reason, the wild-card asterik should also not be used as part of the I argument. Thus in a data file, the line corresponding to the 1st example above would be listed as

```
2 1.0 1.0 2.5
```

If coefficients for type pairs with I not equal J are not set explicitly by a pair\_coeff command, they are inferred from the I,I and J,J settings by mixing rules; see the pair\_modify command for a discussion. Exceptions to the mixing rules of the pair\_modify command are discussed below.

Here are the coefficients specified by the pair\_coeff command for each pair style. Note that when allowed, cutoff arguments are optional; if they are specified for a particular I,J pair they override the global cutoff(s) specified by the pair\_style command.

The units of each coefficient are shown in parenthesis.

---

$$E = Ae^{-r/\rho} - \frac{C}{r^6} \quad r < r_c$$

For styles *buck*, *buck/coul/cut*, and *buck/coul/long*, specify 3, 4, or 5 coefficients:

- A (energy units)
- rho (distance units)
- C (energy–distance<sup>6</sup> units)
- cutoff (distance units)
- cutoff2 (distance units)

The latter 2 coefficients are optional. If not specified, the global LJ and Coulombic cutoffs are used. If only one cutoff is specified, it is used as the cutoff for both LJ and Coulombic interactions for this type pair. If both coefficients are specified, they are used as the LJ and Coulombic cutoffs for this type pair. You cannot specify 2 cutoffs for style *buck*, since it has no Coulombic terms.

For *buck/coul/long* only the LJ cutoff can be specified since a Coulombic cutoff cannot be specified for an individual I,J type pair. All type pairs use the same global Coulombic cutoff specified in the *pair\_style* command.

---

The *dipole* styles are not yet implemented in LAMMPS. They will enable a point dipole and charge to be assigned to each atom and the resulting charge–dipole and dipole–dipole interactions to be computed.

---

$$\begin{aligned} \vec{f} &= (F^C + F^D + F^R)\hat{r}_{ij} & r < r_c \\ F^C &= Aw(r) \\ F^D &= -\gamma w^2(r)(\hat{r}_{ij} \bullet \vec{v}_{ij}) \\ F^R &= \sigma w(r)\alpha(\Delta t)^{-1/2} \\ w(r) &= 1 - r/r_c \end{aligned}$$

For style *dpd*, specify 2 or 3 coefficients:

- A (force units)
- gamma (force/velocity units)
- cutoff (distance units)

The last coefficient is optional. If not specified, the global DPD cutoff is used. Note that sigma is set equal to sqrt(2 T gamma), where T is the temperature set by the *pair\_style* command so it does not need to be specified.

---

$$E_i = F_\alpha \left( \sum_{j \neq i} \rho_\alpha(r_{ij}) \right) + \frac{1}{2} \sum_{j \neq i} \phi_{\alpha\beta}(r_{ij})$$

For style *eam*, potential values are read from a file that is in the DYNAMO single–element *funcfl* format. If

the DYNAMO file was created by a Fortran program, it cannot have "D" values in it for exponents. C only recognizes "e" or "E" for scientific notation.

Note that unlike for other potentials, you do not set cutoffs for EAM potentials in the `pair_style` or `pair_coeff` command; they are specified in the EAM potential files.

For style *eam* you must assign a potential file to each I,I pair of atom types by using a single `pair_coeff` argument:

- filename

Thus the following command

```
pair_coeff *2 1*2 cuu3
```

will read the `cuu3` potential file and use the tabulated Cu values for *F*, *phi*, *rho* that it contains for type pairs 1,1 and 2,2 (type pairs 1,2 and 2,1 are ignored). In effect, this makes atom types 1 and 2 in LAMMPS be Cu atoms. Different single–element files can be assigned to different atom types to model an alloy system. The mixing to create alloy potentials for type pairs with  $I \neq J$  is done automatically the same way that the serial DYNAMO code originally did it; you do not need to specify coefficients for these type pairs.

There are several *funcfl* files in the *potentials* directory of the LAMMPS distribution. A DYNAMO single–element *funcfl* file is formatted as follows:

- line 1: comment (ignored)
- line 2: atomic number, mass, lattice constant, lattice type (e.g. FCC)
- line 3: *Nrho*, *drho*, *Nr*, *dr*, cutoff

On line 2, all values but the mass are ignored by LAMMPS. The mass is in atomic mass units which is converted by LAMMPS to the appropriate internal mass units. On line 3, *Nrho* and *Nr* are the number of tabulated values in the subsequent arrays, *drho* and *dr* are the spacing in density and distance space for the values in those arrays, and the specified cutoff becomes the pairwise cutoff used by LAMMPS for the potential. The units of *dr* are Angstroms; I'm not sure of the units for *drho* – some measure of electron density.

Following the 3 header lines are 3 arrays of tabulated values:

- embedding function *F* (*Nrho* values)
- pair potential function *phi* (*Nr* values)
- density function *rho* (*Nr* values)

The values for each array can be listed as multiple values per line, so long as each array starts on a new line. The individual values are (for example)  $\phi(r)$  for  $r = 0, dr, 2*dr, \dots (Nr-1)*dr$ .

---


$$E_i = F_\alpha \left( \sum_{j \neq i} \rho_\alpha(r_{ij}) \right) + \frac{1}{2} \sum_{j \neq i} \phi_{\alpha\beta}(r_{ij})$$

For style *eam/alloy*, potential values are read from a file that is in the DYNAMO multi–element *setfl* format. If the DYNAMO file was created by a Fortran program, it cannot have "D" values in it for exponents. C only recognizes "e" or "E" for scientific notation.

Only one `pair_coeff` command can be used (one file). DYNAMO *setfl* files contain information for M elements. These are mapped to LAMMPS atom types by specifying N additional arguments after the filename, where N is the number of LAMMPS atom types:

- filename
- N values from 0 to M = mapping of *setfl* elements to atom types

As an example, the *nialhjea* *setfl* file has tabulated EAM values for 3 elements and their alloy interactions: Ni, Al, and H. If your LAMMPS simulation has 4 atoms types and you want the 1st 3 to be Ni, and the 4th to be Al, you would use the following `pair_coeff` command:

```
pair_coeff * * nialhjea 1 1 1 2
```

The 1st 2 arguments must be `**` so as to span all LAMMPS atom types. The first three "1" values map LAMMPS atom types 1,2,3 to the 1st element (Ni) in the *setfl* file. The final "2" value maps LAMMPS atom type 4 to the 2nd element = Al. If a mapping value is "0", the mapping is not performed. This is useful when EAM potentials are part of the *hybrid* pair style, to represent non-EAM atom types.

There is one *setfl* file (*nialhjea*) in the *potentials* directory of the LAMMPS distribution. A DYNAMO multi-element *setfl* file is formatted as follows:

- lines 1,2,3 = comments (ignored)
- line 4: Nelements = # of elements in the file
- line 5: Nrho, drho, Nr, dr, cutoff

The meaning of the values in line 5 is the same as for the *funcfl* file described above. Note that the cutoff is a global value, valid for all pairwise interactions for all element pairings.

Following the 5 header lines are Nelements sections, one for each element, each with the following format:

- line 1 = atomic number, mass, lattice constant, lattice type (e.g. FCC)
- embedding function F (Nrho values)
- density function rho (Nr values)

As with the *funcfl* files, only the mass is used by LAMMPS from the 1st line. The F and rho arrays are unique to a single element and are formatted the same as in a *funcfl* file.

Following the Nelements sections, values for the pair potential phi arrays are listed for all i,j element pairs in the same format as other arrays. Since these interactions are symmetric ( $i,j = j,i$ ) only phi arrays with  $i \geq j$  are listed, in the following order:  $i,j = (1,1), (2,1), (2,2), (3,1), (3,2), (3,3), (4,1), \dots, (Nelements, Nelements)$ . The tabulated values for each phi function are listed in *setfl* files as *r\*phi*, rather than as phi (in *funcfl* files).

---


$$E_i = F_\alpha \left( \sum_{j \neq i} \rho_{\alpha\beta}(r_{ij}) \right) + \frac{1}{2} \sum_{j \neq i} \phi_{\alpha\beta}(r_{ij})$$

For style *eam/fs*, the form of the `pair_coeff` command is exactly the same as for style *eam/alloy*, e.g.

```
pair_coeff * * filename 1 1 1 2
```

where there are N additional arguments after the filename, where N is the number of LAMMPS atom types. The N values determine the mapping of LAMMPS atom types to EAM elements in the file, as described in style *eam/alloy*.

The difference is that files read by *eam/fs* are in a more general format than the DYNAMO *setfl* format read by *eam/alloy*, so that the i,j density functionals for all pairs of elements are included as needed by the Finnis/Sinclair formulation of the EAM.

There is one FS file (nialhjea\_FS) in the *potentials* directory of the LAMMPS distribution. It is formatted as follows:

- lines 1,2,3 = comments (ignored)
- line 4: Nelements = # of elements in the file
- line 5: Nrho, drho, Nr, dr, cutoff

The 5-line header section is identical to an EAM *setfl* file.

Following the header are Nelements sections, one for each element I, each with the following format:

- line 1 = atomic number, mass, lattice constant, lattice type (e.g. FCC)
- embedding function F (Nrho values)
- density function rho for element I at element 1 (Nr values)
- density function rho for element I at element 2
- ...
- density function rho for element I at element Nelement

Following the Nelements sections, values for the pair potential phi arrays are listed in the same manner (r\*phi) as in EAM *setfl* files. Note that the rho arrays in Finnis/Sinclair can be asymmetric (i,j != j,i) so there are Nelements^2 of them listed in the file. But the phi arrays are still symmetric, so only phi arrays for i >= j are listed.

---


$$F = f(\delta/d) (k_n \delta \mathbf{n}_{ij} - m_{\text{eff}} \gamma_n \mathbf{v}_n) + f(\delta/d) (-k_t \delta \Delta \mathbf{s}_t - m_{\text{eff}} \gamma_t \mathbf{v}_t)$$

For styles *gran/hertzian*, *gran/history*, and *gran/no\_history*, there are no individual atom type coefficients that can be set. All global settings are made via the *pair\_style* command.

---

$$\begin{aligned}
E &= LJ(r) & r < r_{\text{in}} \\
&= S(r) * LJ(r) & r_{\text{in}} < r < r_{\text{out}} \\
&= 0 & r > r_{\text{out}} \\
E &= C(r) & r < r_{\text{in}} \\
&= S(r) * C(r) & r_{\text{in}} < r < r_{\text{out}} \\
&= 0 & r > r_{\text{out}} \\
LJ(r) &= 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \\
C(r) &= \frac{C q_i q_j}{\epsilon r} \\
S(r) &= \frac{[r_{\text{out}}^2 - r^2]^2 [r_{\text{out}}^2 + 2r^2 - 3r_{\text{in}}^2]}{[r_{\text{out}}^2 - r_{\text{in}}^2]^3}
\end{aligned}$$

For styles *lj/charmm/coul/charmm*, *lj/charmm/coul/charmm/implicit*, and *lj/charmm/coul/long*, specify 2 or 4 coefficients:

- epsilon (energy units)
- sigma (distance units)
- epsilon\_14 (energy units)
- sigma\_14 (distance units)

Note that sigma is defined in the LJ formula as the zero-crossing distance for the potential, not as the energy minimum at  $2^{1/6}$  sigma.

The latter 2 coefficients are optional. If they are specified, they are used in the Lennard–Jones formula between 2 atoms of these types which are also first and fourth atoms in any dihedral. No cutoffs are specified because this CHARMM force field does not allow varying cutoffs for individual atom pairs; all pairs use the global cutoff(s) specified in the pair\_style command.

$$E = \epsilon \left[ 2 \left( \frac{\sigma}{r} \right)^9 - 3 \left( \frac{\sigma}{r} \right)^6 \right] \quad r < r_c$$

For styles *lj/class2*, *lj/class2/coul/cut*, and *lj/class2/coul/long*, specify 2, 3, or 4 coefficients:

- epsilon (energy units)
- sigma (distance units)
- cutoff1 (distance units)
- cutoff2 (distance units)

The latter 2 coefficients are optional. If not specified, the global class 2 and Coulombic cutoffs are used. If only one cutoff is specified, it is used as the cutoff for both class 2 and Coulombic interactions for this type pair. If both coefficients are specified, they are used as the class 2 and Coulombic cutoffs for this type pair. You cannot specify 2 cutoffs for style *lj/class2*, since it has no Coulombic terms.

For *lj/class2/coul/long* only the class 2 cutoff can be specified since a Coulombic cutoff cannot be specified for an individual I,J type pair. All type pairs use the same global Coulombic cutoff specified in the *pair\_style* command.

---

$$E = 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \quad r < r_c$$

$$E = \frac{Cq_iq_j}{\epsilon r} \quad r < r_c$$

$$E = \frac{Cq_iq_j}{\epsilon r} \exp(-\kappa r) \quad r < r_c$$

For styles *lj/cut*, *lj/cut/coul/cut*, *lj/cut/coul/debye*, *lj/cut/coul/long*, and *lj/cut/coul/long/tip4p* specify 2, 3, or 4 coefficients:

- epsilon (energy units)
- sigma (distance units)
- cutoff1 (distance units)
- cutoff2 (distance units)

Note that sigma is defined in the LJ formula as the zero-crossing distance for the potential, not as the energy minimum at  $2^{1/6}$  sigma.

The latter 2 coefficients are optional. If not specified, the global LJ and Coulombic cutoffs are used. If only one cutoff is specified, it is used as the cutoff for both LJ and Coulombic interactions for this type pair. If both coefficients are specified, they are used as the LJ and Coulombic cutoffs for this type pair. You cannot specify 2 cutoffs for style *lj/cut*, since it has no Coulombic terms.

For *lj/cut/coul/long* and *lj/cut/coul/long/tip4p* only the LJ cutoff can be specified since a Coulombic cutoff cannot be specified for an individual I,J type pair. All type pairs use the same global Coulombic cutoff specified in the *pair\_style* command.

---

$$E = 4\epsilon \left[ \left( \frac{\sigma}{r - \Delta} \right)^{12} - \left( \frac{\sigma}{r - \Delta} \right)^6 \right] \quad r < r_c + \Delta$$

For style *lj/expand*, specify 3 or 4 coefficients:

- epsilon (energy units)
- sigma (distance units)
- delta (distance units)
- cutoff (distance units)

The delta values can be positive or negative. Note that the cutoff does not include the delta distance. I.e. the

actual force cutoff is the sum of cutoff + delta.

The last coefficient is optional. If not specified, the global LJ cutoff is used.

---

$$E = 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \quad r < r_{in}$$

$$F = C1 + C2(r - r_{in}) + C3(r - r_{in})^2 + C4(r - r_{in})^3 \quad r_{in} < r < r_c$$

For style *lj/smooth*, specify 2 or 4 coefficients:

- epsilon (energy units)
- sigma (distance units)
- Rin (distance units)
- cutoff (distance units)

The last 2 coefficients are optional. If not specified, the global Rin and cutoff are used. Rin cannot be 0.0. If Rin = cutoff, then no force smoothing is performed for this type pair; the standard LJ formula is used.

---

$$E = D_0 \left[ e^{-2\alpha(r-r_0)} - 2e^{-\alpha(r-r_0)} \right] \quad r < r_c$$

For style *morse*, specify 3 or 4 coefficients:

- D0 (energy units)
- alpha (1/distance units)
- r0 (distance units)
- cutoff (distance units)

The last coefficient is optional. If not specified, the global morse cutoff is used.

---

$$E = A \left[ 1 + \cos \left( \frac{\pi r}{r_c} \right) \right] \quad r < r_c$$

For style *soft*, specify 2 or 3 coefficients:

- Astart (energy units)
- Astop (energy units)
- cutoff (distance units)

Astart and Astop are the values of the prefactor at the start and end of the next run. At intermediate times the value of A will be ramped between these 2 values. Note that before performing a 2nd run, you will want to adjust the values of Astart and Astop for all type pairs, or switch to a new pair style.

The last coefficient is optional. If not specified, the global soft cutoff is used.

---

For style *table*, specify 2 or 3 coefficients:



- filename
- keyword
- cutoff (distance units)

The filename specifies a file containing tabulated energy and force values. The keyword specifies a section of the file. The cutoff is an optional coefficient. If not specified, the outer cutoff in the table itself (see below) will be used to build an interpolation table that extend to the largest tabulated distance. If specified, only file values up to the cutoff are used to create the interpolation table.

The format of a tabulated file is as follows (without the parenthesized comments):

```
# Morse potential for Fe      (one or more comment or blank lines)

MORSE_FE                      (keyword is first text on line)
N 500 R 1.0 10.0              (N, R, RSQ, BITMAP, FPRIME parameters)
                               (blank)
1 1.0 25.5 102.34             (index, r, energy, force)
2 1.02 23.4 98.5
...
500 10.0 0.001 0.003
```

A section begins with a non-blank line whose 1st character is not a "#"; blank lines or lines starting with "#" can be used as comments between sections. The first line begins with a keyword which identifies the section. The line can contain additional text, but the initial text must match the argument specified in the `pair_coeff` command. The next line lists (in any order) one or more parameters for the table. Each parameter is a keyword followed by one or more numeric values.

The parameter "N" is required; its value is the number of table entries that follow. All other parameters are optional. If "R" or "RSQ" or "BITMAP" does not appear, then the distances in each line of the table are used as-is to perform spline interpolation. In this case, the table values can be spaced in  $r$  uniformly or however you wish to position table values in regions of large gradients.

If used, the parameters "R" or "RSQ" are followed by 2 values  $rlo$  and  $rhi$ . If specified, the distance associated with each energy and force value is computed from these 2 values (at high accuracy), rather than using the (low-accuracy) value listed in each line of the table. For "R", distances uniformly spaced between  $rlo$  and  $rhi$  are computed; for "RSQ", squared distances uniformly spaced between  $rlo*rlo$  and  $rhi*rhi$  are computed.

If used, the parameter "BITMAP" is also followed by 2 values  $rlo$  and  $rhi$ . These values, along with the "N" value determine the ordering of the N lines that follow and what distance is associated with each. This ordering is complex, so it is not documented here, since this file is typically produced by the `pair_write` command with its `bitmap` option. When the table is in BITMAP format, the "N" parameter in the file must be equal to  $2^M$  where M is the value specified in the `pair_style` command. Also, a cutoff parameter cannot be used as an optional 3rd argument in the `pair_coeff` command; the entire table extent as specified in the file must be used.

If used, the parameter "FPRIME" is followed by 2 values  $fplo$  and  $fphi$  which are the derivative of the force at the innermost and outermost distances listed in the table. These values are needed by the spline construction routines. If not specified by the "FPRIME" parameter, they are estimated (less accurately) by the first 2 and last 2 force values in the table. This parameter is not used by BITMAP tables.

Following a blank line, the next N lines list the tabulated values. On each line, the 1st value is the index from 1 to N, the 2nd value is  $r$  (in distance units), the 3rd value is the energy (in energy units), and the 4th is the

force (in force units). The  $r$  values must increase from one line to the next (unless the BITMAP parameter is specified).

Note that one file can contain many sections, each with a tabulated potential. LAMMPS reads the file section by section until it finds one that matches the specified keyword.

---

$$E = A \frac{e^{-\kappa r}}{r} \quad r < r_c$$

For style *yukawa*, specify 1 or 2 coefficients:

- A (energy units)
- cutoff (distance units)

The last coefficient is optional. If not specified, the global yukawa cutoff is used.

---

For style *hybrid*, each `pair_coeff` command assigns one of the sub-styles specified in the `pair_style` command to a set of atom type pairs. The arguments of the `pair_coeff` command are the same as they would be for the sub-style itself, except that an additional argument is added (after the type pairs) which specifies which sub-style is being used. For example, consider a simulation with 3 atom types: types 1 and 2 are Ni atoms, type 3 are LJ atoms with charges. The following commands would set up the hybrid simulation:

```
atom_style hybrid eam charge
pair_style hybrid eam lj/cut/coul/cut 10.0 lj/cut 8.0
pair_coeff 1*2 1*2 eam niu3
pair_coeff 3 3 lj/cut/coul/cut 1.0 1.0
pair_coeff 1*2 3 lj/cut 0.5 1.2
```

The `atom_style hybrid` command is needed because atoms in the simulation will have both EAM and charge attributes.

---

### Restrictions:

This command must come after the simulation box is defined by a `read_data`, `read_restart`, or `create_box` command.

### Related commands:

`pair_style`, `pair_modify`, `read_data`, `read_restart`, `pair_write`

**Default:** none

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---

## pair\_modify command

### Syntax:

```
pair_modify keyword value ...
```

- one or more keyword/value pairs may be listed
- keyword = *shift* or *mix*

```

shift value = yes or no
mix value = geometric or arithmetic or sixthpower
table value = N
      2^N = # of values in table
tabinner value = cutoff
      cutoff = inner cutoff at which to begin table (distance units)

```

### Examples:

```

pair_modify shift yes
pair_modify mix arithmetic
pair_modify table 12

```

### Description:

Modify the parameters of the currently defined pair style. Not all parameters are relevant to all pair styles.

The *shift* keyword determines whether the Lennard–Jones potential is shifted at its cutoff to 0.0. If so, this adds an energy term to each pairwise interaction which will be printed in the thermodynamic output, but does not affect atom dynamics (forces). Pair styles that are already 0.0 at their cutoff such as *lj/charmm/coul/charmm* are not affected by this setting.

The *mix* keyword affects how Lennard–Jones coefficients for epsilon and sigma are generated for interactions between atoms of type I and J, when  $I \neq J$ . ( $I = J$  coefficients are set explicitly in the data file or input script.) The `pair_coeff` command can be used in the input script to specify epsilon/sigma for a specific I,J pairing, which overrides the setting of the *mix* keyword. In each case, the LJ cutoff is mixed the same way as sigma.

These are the formulas used by the 3 *mix* options:

#### *geometric*

```

epsilon_ij = sqrt(epsilon_i * epsilon_j)
sigma_ij = sqrt(sigma_i * sigma_j)

```

#### *arithmetic*

```

epsilon_ij = sqrt(epsilon_i * epsilon_j)
sigma_ij = (sigma_i + sigma_j) / 2

```

#### *sixthpower*

```

epsilon_ij = (2 * sqrt(epsilon_i*epsilon_j) * sigma_i^3 * sigma_j^3) /
              (sigma_i^6 + sigma_j^6)
sigma_ij = ((sigma_i**6 + sigma_j**6) / 2) ^ (1/6)

```

Style *soft* only uses a pre-factor coefficient, which is always mixed geometrically, regardless of the *mix* setting. The *charmm* styles are always mixed arithmetically, regardless of the *mix* setting. The *class2* styles are always mixed as a sixthpower, regardless of the *mix* setting, except that the cutoff is mixed according to the *mix* setting. Style *lj/expand* always mixes its delta coefficient using the rule

```

delta_ij = (delta_i + delta_j) / 2

```

The *table* keyword applies to pair styles with a long-range Coulombic term (lj/cut/coul/long and lj/charmm/coul/long). If N is non-zero, a table of length  $2^N$  is pre-computed for forces and energies, which can shrink their computational cost by up to a factor of 2. The table is indexed via a bit-mapping technique ([Wolff](#)) and a linear interpolation is performed between adjacent table values. In our experiments with different table styles (lookup, linear, spline), this method typically gave the best performance in terms of speed and accuracy.

The choice of table length is a tradeoff in accuracy versus speed. A larger N yields more accurate force computations, but requires more memory which can slow down the computation due to cache misses. A reasonable value of N is between 8 and 16. The default value of 12 (table of length 4096) gives approximately the same accuracy as the no-table (N = 0) option. For N = 0, forces and energies are computed directly, using a polynomial fit for the needed erfc() function evaluation, which is what earlier versions of LAMMPS did. Values greater than 16 typically slow down the simulation and will not improve accuracy; values from 1 to 8 give unreliable results.

The *tabinner* keyword sets an inner cutoff above which the pairwise computation is done by table lookup (if tables are invoked). The smaller this value is set, the less accurate the table becomes (for a given number of table values), which can require use of larger tables. The default cutoff value is sqrt(2.0) distance units which means nearly all pairwise interactions are computed via table lookup for simulations with "real" units, but some close pairs may be computed directly (non-table) for simulations with "lj" units.

**Restrictions:** none

**Related commands:**

[pair\\_style](#), [pair\\_coeff](#)

**Default:**

The option defaults are shift = no, mix = arithmetic (for lj/charmm pair styles), mix = geometric (for other pair styles), table = 12, and tabinner = sqrt(2.0).

([Wolff](#)) Wolff and Rudd, Comp Phys Comm, 120, 200–32 (1999).

[LAMMPS WWW Site](#) – [LAMMPS Documentation](#) – [LAMMPS Commands](#)

## pair\_style command

**Syntax:**

```
pair_style style args
```

- style = one of the following
  - ◆ none
  - ◆ buck or buck/coul/cut or buck/coul/long
  - ◆ dipole/cut or dipole/long
  - ◆ dpd
  - ◆ eam or eam/alloy or eam/fs
  - ◆ gran/hertzian or gran/history or gran/no\_history

- ◆ *lj/charmm/coul/charmm* or *lj/charmm/coul/charmm/implicit* or *lj/charmm/coul/long*
- ◆ *lj/class2* or *lj/class2/coul/cut* or *lj/class2/coul/long*
- ◆ *lj/cut* or *lj/cut/coul/cut* or *lj/cut/coul/debye* or *lj/cut/coul/long* or *lj/cut/coul/long/tip4p*
- ◆ *lj/expand*
- ◆ *lj/smooth*
- ◆ *morse*
- ◆ *soft*
- ◆ *table*
- ◆ *yukawa*
- ◆ *hybrid*

- *args* = list of arguments for a particular style

```

none args = none
buck args = cutoff
buck/coul/cut args = cutoff (cutoff2)
buck/coul/long args = cutoff (cutoff2)
    cutoff = cutoff for Buckingham (and Coulombic if only 1 arg)
    cutoff2 = cutoff for Coulombic (optional)
dipole/cut args = cutoff (cutoff2)
dipole/long args = cutoff (cutoff2)
    cutoff = cutoff for Lennard Jones (and Coulombic if only 1 arg)
    cutoff2 = cutoff for Coulombic (optional)
dpd args = T cutoff seed
    T = temperature (temperature units)
    cutoff = cutoff for DPD interactions
    seed = random # seed (integer > 0 and <900000000)
eam args = none
eam/alloy args = none
eam/fs args = none
gran/hertzian args = Kn, gamma_n, xmu, dampflag
gran/history args = Kn, gamma_n, xmu, dampflag
gran/no_history args = Kn, gamma_n, xmu, dampflag
    Kn = spring constant for particle repulsion (mg/d units where
        m is mass, g is the gravitational constant,
        d is diameter of a particle)
    gamma_n = damping coefficient for normal direction collisions
              (sqrt(g/d) units)
    xmu = friction coefficient or static yield criterion
    dampflag = flag (0/1) for whether to (no/yes) include tangential damping
lj/charmm/coul/charmm args = inner outer (inner2) (outer2)
lj/charmm/coul/charmm/implicit args = inner outer (inner2) (outer2)
lj/charmm/coul/long args = inner outer (cutoff)
    inner, outer = switching cutoffs for LJ (and Coulombic if only 2 args)
    inner2, outer2 = switching cutoffs for Coulombic (optional)
    cutoff = cutoff for Coulombic (optional, outer is Coulombic cutoff if only 2 args)
lj/class2 args = cutoff
lj/class2/coul/cut args = cutoff (cutoff2)
lj/class2/coul/long args = cutoff (cutoff2)
    cutoff = cutoff for class2 (and Coulombic if only 1 arg)
    cutoff2 = cutoff for Coulombic (optional)
lj/cut args = cutoff
lj/cut/coul/cut args = cutoff (cutoff2)
lj/cut/coul/debye args = kappa cutoff (cutoff2)
lj/cut/coul/long args = cutoff (cutoff2)
    cutoff = cutoff for Lennard Jones (and Coulombic if only 1 arg)
    cutoff2 = cutoff for Coulombic (optional)
    kappa = Debye length (inverse distance units)
lj/cut/coul/long/tip4p args = otype htype btype atype qdist cutoff (cutoff2)
    otype,htype = atom types for TIP4P O and H
    btype,atype = bond and angle types for TIP4P waters

```

```

    qdist = distance from O atom to massless charge (distance units)
    cutoff = cutoff for Lennard Jones (and Coulombic if only 1 arg)
    cutoff2 = cutoff for Coulombic (optional)
lj/expand args = cutoff
    cutoff = cutoff for expanded Lennard-Jones interactions
lj/smooth args = inner cutoff
    inner = inner cutoff beyond which force smoothing will be applied
    cutoff = cutoff for Lennard-Jones interactions
morse args = cutoff
    cutoff = cutoff for Morse interactions
soft = cutoff
    cutoff = cutoff for soft interactions
table args = style N
    style = lookup or linear or spline or bitmap = method of interpolation
    N = use N values in lookup, linear, spline tables
    N = use 2^N values in bitmap tables
yukawa args = kappa cutoff
    kappa = screening length (inverse distance units)
    cutoff = cutoff for Yukawa interactions
hybrid args = list of one or more styles with their args

```

## Examples:

```

pair_style none
pair_style eam/alloy
pair_style gran/history 200000.0 0.5 1.0 1
pair_style lj/charmm/coul/charmm 10.0 10.3
pair_style lj/charmm/coul/charmm/implicit 10.0
pair_style lj/charmm/coul/long 10.0
pair_style lj/cut 2.5
pair_style lj/cut/coul/cut 10.0 8.0
pair_style lj/cut/coul/debye 1.5 3.0
pair_style lj/cut/coul/long 12.0
pair_style lj/cut/coul/long/tip4p 1 2 7 8 12.0
pair_style lj/expand 2.5
pair_style lj/smooth 2.2 2.5
pair_style lj/class2 8.0
pair_style soft 2.0
pair_style dpd 1.0 1.0 48279
pair_style table linear 1000
pair_style table bitmap 12
pair_style hybrid lj/charmm/coul/long 10.0 eam

```

## Description:

Set the formula(s) LAMMPS will use to computing pairwise interactions. In LAMMPS, a pairwise force field includes all pairwise interactions (Lennard Jones, Coulombic, etc), so there is a range of style choices that encompass combinations of multiple kinds of interactions.

The coefficients for the formulas for each atom type pair are set by the pair\_coeff command or read from a file by the read\_data or read\_restart commands. Mixing and shifting of the interaction potentials is discussed in the documentation for the pair\_modify command.

The cutoff arguments set global cutoffs for all atom type pairs. The global value can be overridden by the pair\_coeff command for a specific pair. The pair style settings (including global cutoffs) can be changed by a subsequent pair\_style command using the same style. This will reset the cutoffs for all atom type pairs, including those previously set explicitly by a pair\_coeff command. The exceptions to this are that pair\_style table and hybrid settings cannot be reset. A new pair\_style command for these styles will wipe out all

previously specified `pair_coeff` values.

All cutoff arguments are in distance units. The distance(s) can be smaller or larger than the dimensions of the simulation box.

In the formulas to follow,  $E$  is the energy of a pairwise interaction between two atoms separated by a distance  $r$ . The force between the atoms is the negative derivative of this expression.

---

Style *none* turns off pairwise interactions.

With this choice, the force cutoff is 0.0, which means that only atoms within the neighbor skin distance (see the `neighbor` command) are communicated between processors. You must insure the skin distance is large enough to acquire atoms needed for computing bonds, angles, etc.

A pair style of *none* will also prevent pairwise neighbor lists from being built. However if the `neighbor` style is *bin*, data structures for binning are still allocated. If the neighbor skin distance is small, then these data structures can consume a large amount of memory. So you should either set the neighbor style to *nsq* or set the skin distance to a larger value.

---

The *buck* styles compute a Buckingham potential (exp/6 instead of Lennard–Jones 12/6) given by

$$E = Ae^{-r/\rho} - \frac{C}{r^6} \quad r < r_c$$

where  $A$ ,  $\rho$ , and  $C$  are coefficients defined for each pair of atom types.  $R_c$  is the cutoff.

The *buck/coul/cut* and *buck/coul/long* styles add a Coulombic term as described in the *lj/cut* styles.

---

The *dipole* styles are not yet implemented in LAMMPS. They will enable a point dipole and charge to be assigned to each atom and the resulting charge–dipole and dipole–dipole interactions to be computed.

---

Style *dpd* computes a force field for dissipative particle dynamics (DPD) following the exposition in [\(Groot\)](#). The force on atom  $I$  due to atom  $J$  is given as a sum of 3 terms

$$\begin{aligned}\vec{f} &= (F^C + F^D + F^R)\hat{r}_{ij} & r < r_c \\ F^C &= Aw(r) \\ F^D &= -\gamma w^2(r)(\hat{r}_{ij} \bullet \vec{v}_{ij}) \\ F^R &= \sigma w(r)\alpha(\Delta t)^{-1/2} \\ w(r) &= 1 - r/r_c\end{aligned}$$

where  $F^C$  is a conservative force,  $F^D$  is a dissipative force, and  $F^R$  is a random force.  $\hat{r}_{ij}$  is a unit vector in the direction  $\mathbf{r}_i - \mathbf{r}_j$ ,  $\mathbf{v}_{ij}$  is the vector difference in velocities of the two atoms  $= \mathbf{v}_i - \mathbf{v}_j$ ,  $\alpha$  is a Gaussian random number with zero mean and unit variance,  $\Delta t$  is the timestep size, and  $w(r)$  is a weighting factor that varies between 0 and 1.  $A$  and  $\gamma$  are coefficients defined for each pair of atom types.  $R_c$  is the cutoff.  $\sigma$  is set equal to  $\sqrt{2 T \gamma}$ , where  $T$  is a parameter in the `pair_style` command.

---

Style *eam* computes pairwise interactions for metals and metal alloys using embedded-atom method (EAM) potentials [\(Daw\)](#). The total energy  $E_i$  of an atom  $I$  is given by

$$E_i = F_\alpha \left( \sum_{j \neq i} \rho_\alpha(r_{ij}) \right) + \frac{1}{2} \sum_{j \neq i} \phi_{\alpha\beta}(r_{ij})$$

where  $F$  is the embedding energy which is a function of the atomic electron density  $\rho$ ,  $\phi$  is a pair potential interaction, and  $\alpha$  and  $\beta$  are the element types of atoms  $I$  and  $J$ . The multi-body nature of the EAM potential is a result of the embedding energy term. Both summations in the formula are over all neighbors  $J$  of atom  $I$  within the cutoff distance.

The cutoff distance and the tabulated values of the functionals  $F$ ,  $\rho$ , and  $\phi$  are listed in one or more files which are specified by the `pair_coeff` command. These are ASCII text files in a DYNAMO-style format which is described in the documentation for the `pair_coeff` command. DYNAMO is a serial MD code. Several DYNAMO potential files for different metals are included in the "potentials" directory of the LAMMPS distribution.

**IMPORTANT NOTE:** The *eam* style reads single-element EAM potentials in the DYNAMO *funcfl* format. Single element or alloy systems can be modeled with *funcfl* files and style *eam*; for the alloy case LAMMPS mixes the single-element potentials to produce alloy potentials the same way that DYNAMO does. Alternatively, DYNAMO *setfl* files can be used by LAMMPS to model alloy systems by invoking the *eam/alloy* style as described below. *Setfl* files require no mixing as they specify alloy interactions explicitly.

---

Style *eam/alloy* computes pairwise interactions using the same formula as style *eam*. However the associated `pair_coeff` command reads a DYNAMO *setfl* file instead of a *funcfl* file. *Setfl* files can be used to model a single-element or alloy system. In the alloy case, as explained above, *setfl* files contain explicit tabulated values for alloy interactions. Thus they allow more generality than *funcfl* files for modeling alloys.

---

Style *eam/fs* computes pairwise interactions for metals and metal alloys using a generalized form of EAM potentials due to Finnis and Sinclair [\(Finnis\)](#). The total energy  $E_i$  of an atom  $I$  is given by

$$E_i = F_\alpha \left( \sum_{j \neq i} \rho_{\alpha\beta}(r_{ij}) \right) + \frac{1}{2} \sum_{j \neq i} \phi_{\alpha\beta}(r_{ij})$$

This has the same form as the EAM formula above, except that  $\rho$  is now a functional specific to the atomic types of both atoms  $I$  and  $J$ , so that different elements can contribute differently to the total electron density at an atomic site depending on the identity of the element at that atomic site.

The associated `pair_coeff` command for style *eam/fs* reads a DYNAMO *setfl* file that has been extended to include additional `rho_alpha_beta` arrays of tabulated values. The details are given in the `pair_coeff` documentation.

A discussion of how FS EAM differs from conventional EAM alloy potentials is given in [\(Ackland1\)](#). An example of such a potential is the same author's Fe-P FS potential [\(Ackland2\)](#). Note that while FS potentials always specify the embedding energy with a square root dependence on the total density, the implementation in LAMMPS does not require that; the user can tabulate any functional form he desires in the FS potential files.



---

The *gran* styles use the following formula (Silbert) for frictional force between two granular particles that are a distance  $r$  apart when  $r$  is less than the contact distance  $d$ .

$$F = f(\delta/d) (k_n \delta \mathbf{n}_{ij} - m_{\text{eff}} \gamma_n \mathbf{v}_n) + f(\delta/d) (-k_t \delta \Delta \mathbf{s}_t - m_{\text{eff}} \gamma_t \mathbf{v}_t)$$

The 1st term is a normal force and the 2nd term is a tangential force. The other quantites are as follows:

- $\delta = d - r$
- $f(x) = 1$  for Hookean contacts used in pair styles *history* and *no\_history*
- $f(x) = \text{sqrt}(x)$  for pair style *hertzian*
- $K_n$  = elastic constant for normal contact (listed above)
- $K_t$  = elastic constant for tangential contact = 2/7 of  $K_n$
- $\gamma_n$  = viscoelastic constants for normal contact (listed above)
- $\gamma_t$  = viscoelastic constants for tangential contact = 1/2 of  $\gamma_n$
- $m_{\text{eff}} = M_i M_j / (M_i + M_j)$  = effective mass of 2 particles of mass  $M_i$  and  $M_j$
- $\Delta \mathbf{s}_t$  = tangential displacement vector between the 2 spherical particles which is truncated to satisfy a frictional yield criterion
- $\mathbf{n}$  = a unit vector along the line connecting the centers of the 2 particles
- $\mathbf{v}_n$  = normal component of the relative velocity of the 2 particles
- $\mathbf{v}_t$  = tangential component of the relative velocity of the 2 particles

See the citation for more discussion of the granular potentials.

---

The *lj/charmm* styles compute LJ and Coulombic interactions with an additional switching function  $S(r)$  that ramps the energy and force smoothly to zero between an inner and outer cutoff. It is a widely used option in the CHARMM MD code.

$$\begin{aligned}
 E &= LJ(r) & r < r_{\text{in}} \\
 &= S(r) * LJ(r) & r_{\text{in}} < r < r_{\text{out}} \\
 &= 0 & r > r_{\text{out}} \\
 E &= C(r) & r < r_{\text{in}} \\
 &= S(r) * C(r) & r_{\text{in}} < r < r_{\text{out}} \\
 &= 0 & r > r_{\text{out}} \\
 LJ(r) &= 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \\
 C(r) &= \frac{C q_i q_j}{\epsilon r} \\
 S(r) &= \frac{[r_{\text{out}}^2 - r^2]^2 [r_{\text{out}}^2 + 2r^2 - 3r_{\text{in}}^2]}{[r_{\text{out}}^2 - r_{\text{in}}^2]^3}
 \end{aligned}$$

Both the LJ and Coulombic terms require an inner and outer cutoff. They can be the same for both formulas or different depending on whether 2 or 4 arguments are used in the pair\_style command. In each case, the inner cutoff distance must be less than the outer cutoff. It is typical to make the difference between the 2 cutoffs about 1.0 Angstrom.

Style *lj/charmm/coul/charmm/implicit* computes the same formulas as style *lj/charmm/coul/charmm* except that an additional  $1/r$  term is included in the Coulombic formula. The Coulombic energy thus varies as  $1/r^2$ . This is effectively a distance-dependent dielectric term which is a simple model for an implicit solvent with additional screening. It is designed for use in a simulation of an unsolvated biomolecule (no explicit water molecules).

Style *lj/charmm/coul/long* computes the same formulas as style *lj/charmm/coul/charmm* except that an additional damping factor is applied to the Coulombic term, as in the discussion for style *lj/cut/coul/long*. Only one Coulombic cutoff is specified for *lj/charmm/coul/long*; if only 2 arguments are used in the *pair\_style* command, then the outer LJ cutoff is used as the single Coulombic cutoff.

---

The *lj/class2* styles compute a 6/9 Lennard–Jones potential given by

$$E = \epsilon \left[ 2 \left( \frac{\sigma}{r} \right)^9 - 3 \left( \frac{\sigma}{r} \right)^6 \right] \quad r < r_c$$

where epsilon and sigma are coefficients defined for each pair of atom types.  $r_c$  is the cutoff.

The *lj/class2/coul/cut* and *lj/class2/coul/long* styles add a Coulombic term as described in the *lj/cut* styles.

---

The *lj/cut* styles compute the standard 6/12 Lennard–Jones potential, given by

$$E = 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \quad r < r_c$$

where epsilon and sigma are coefficients defined for each pair of atom types.  $r_c$  is the cutoff.

Style *lj/cut/coul/cut* adds a Coulombic pairwise interaction given by

$$E = \frac{Cq_iq_j}{\epsilon r} \quad r < r_c$$

where C is an energy–conversion constant,  $Q_i$  and  $Q_j$  are the charges on the 2 atoms, and epsilon is the dielectric constant which can be set by the *dielectric* command. If one cutoff is specified in the *pair\_style* command, it is used for both the LJ and Coulombic terms. If two cutoffs are specified, they are used as cutoffs for the LJ and Coulombic terms respectively.

Style *lj/cut/coul/debye* adds an additional  $\exp()$  damping factor to the Coulombic term, given by

$$E = \frac{Cq_iq_j}{\epsilon r} \exp(-\kappa r) \quad r < r_c$$

where Kappa is the Debye length. This potential is another way to mimic the screening effect of a polar solvent.

Style *lj/cut/coul/long* computes the same Coulombic interactions as style *lj/cut/coul/cut* except that an additional damping factor is applied to the Coulombic term so it can be used in conjunction with the kspc style command and its *ewald* or *pppm* option. The Coulombic cutoff specified for this style means that pairwise interactions within this distance are computed directly; interactions outside that distance are computed in K-space.

Style *lj/cut/coul/long/tip4p* implements the TIP4P water model of (Jorgensen), which introduces a massless site located a short distance away from the oxygen atom along the bisector of the HOH angle. The atomic types of the oxygen and hydrogen atoms, the bond and angle types for OH and HOH interactions, and the distance to the massless charge site are specified as pair\_style arguments. See the howto section for more information on how to use this pair style.

Style *lj/expand* computes a LJ interaction with a distance shifted by delta

$$E = 4\epsilon \left[ \left( \frac{\sigma}{r - \Delta} \right)^{12} - \left( \frac{\sigma}{r - \Delta} \right)^6 \right] \quad r < r_c + \Delta$$

The epsilon, sigma, and delta coefficients are defined for each pair of atom types. Rc is the cutoff.

Style *lj/smooth* computes a LJ interaction with a force smoothing applied between the inner and outer cutoff.

$$\begin{aligned} E &= 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] & r < r_{in} \\ F &= C1 + C2(r - r_{in}) + C3(r - r_{in})^2 + C4(r - r_{in})^3 & r_{in} < r < r_c \end{aligned}$$

The polynomial coefficients C1, C2, C3, C4 are computed by LAMMPS to cause the force to vary smoothly from Rin to Rc. At Rin the force and its 1st derivative will match the unsmoothed LJ formula. At Rc the force and its 1st derivative will be 0.0. IMPORTANT NOTE: this force smoothing causes the energy to be discontinuous both in its values and 1st derivative. This can lead to poor energy conservation. Plot the energy and force resulting from this formula via the pair write command to see the effect.

The epsilon and sigma are defined for each pair of atom types. Rin is the inner cutoff; Rc is the outer cutoff. If Rin = Rc, then no force smoothing is performed; the standard LJ formula is used unless the pair coeff settings override the cutoffs for a particular type pair.

Style *morse* computes pairwise interactions with the formula

$$E = D_0 \left[ e^{-2\alpha(r-r_0)} - 2e^{-\alpha(r-r_0)} \right] \quad r < r_c$$

where D0, alpha, and r0 are coefficients defined for each pair of atom types. Rc is the cutoff.

Style *soft* is useful for pushing apart overlapping atoms, since it does not blow up as r goes to 0. It computes a pairwise interaction as

$$E = A \left[ 1 + \cos \left( \frac{\pi r}{r_c} \right) \right] \quad r < r_c$$

where A is a pre-factor that varies in time from the start to the end of the run. Starting and ending values for A are specified by the pair\_coeff or read\_data command. Rc is the cutoff.

Style *table* creates interpolation tables of length *N* from pair potential and force values listed in a file(s) as a function of distance. The files are read by the pair\_coeff command which also describes the file format.

The interpolation tables are created by fitting cubic splines to the file values and interpolating energy and force values at each of *N* distances. During a simulation, these tables are used to interpolate energy and force values as needed. The interpolation is done in one of 4 styles: *lookup*, *linear*, *spline*, or *bitmap*.

For the *lookup* style, the distance between 2 atoms is used to find the nearest table entry, which is the energy or force.

For the *linear* style, the distance is used to find 2 surrounding table values from which an energy or force is computed by linear interpolation.

For the *spline* style, a cubic spline coefficients are computed and stored each of the *N* values in the table. The pair distance is used to find the appropriate set of coefficients which are used to evaluate a cubic polynomial which computes the energy or force.

For the *bitmap* style, the N means to create interpolation tables that are 2<sup>N</sup> in length. The pair distance is used to index into the table via a fast bit-mapping technique (Wolff) and a linear interpolation is performed between adjacent table values.

Style *yukawa* computes pairwise interactions with the formula

$$E = A \frac{e^{-\kappa r}}{r} \quad r < r_c$$

where A is a coefficient defined for each pair of atom types. Rc is the cutoff.

The *hybrid* style enables the use of multiple pair styles in one simulation. A pair style can be assigned to each pair of atom types via the pair\_coeff command.

For example, a metal on a LJ surface could be computed where the metal atoms interact with each other via a *eam* potential, the surface atoms interact with each other via a *lj/cut* potential, and the metal/surface interaction is also via a *lj/cut* potential.

All pair styles that will be used must be listed in the `pair_style hybrid` command (in any order). Each sub-style is listed with its arguments, as illustrated in the last example above.

### Restrictions:

This command must be used before any coefficients are set by the pair\_coeff, read\_data, or read\_restart

commands.

The hybrid style cannot include any of the *gran* styles in its list of styles to use. Only one *coul/long* style can be used in the list of hybrid styles.

Some pair styles are part of specific packages. They are only enabled if LAMMPS was built with that package. See the [Making LAMMPS](#) section for more info.

The *gran/hertzian*, *gran/history*, and *gran/no\_history* styles are part of the "granular" package. The *lj/charmm/coul/charmm* and *lj/charmm/coul/charmm/implicit* styles are part of the "molecule" package. The *lj/cut/coul/long* and *lj/charmm/coul/long* styles are part of the "kspace" package. The *eam* styles are part of the "metal" package. The *dpd* style is part of the "dpd" package.

On some 64-bit machines, compiling with `-O3` appears to break the Coulombic tabling option used by the *lj/cut/coul/long* and *lj/charmm/coul/long* styles. See the "Additional build tips" section of the [Making LAMMPS](#) documentation pages for workarounds on this issue.

#### Related commands:

[pair coeff](#), [read data](#), [pair modify](#), [kspace style](#), [dielectric](#), [pair write](#)

#### Default:

```
pair_style none
```

---

**(Ackland1)** Ackland, Condensed Matter (2005).

**(Ackland2)** Ackland, Mendelev, Srolovitz, Han and Barashev, Journal of Physics: Condensed Matter, 16, S2629 (2004).

**(Daw)** Daw, Baskes, Phys Rev Lett, 50, 1285 (1983). Daw, Baskes, Phys Rev B, 29, 6443 (1984).

**(Finnis)** Finnis, Sinclair, Philosophical Magazine A, 50, 45 (1984).

**(Groot)** Groot, Warren, J Chem Phys, 107, 4423 (1997).

**(Jorgensen)** Jorgensen, Chandrasekhar, Madura, Impey, Klein, J Chem Phys, 79, 926 (1983).

**(Silbert)** Silbert, Ertas, Grest, Halsey, Levine, Plimpton, Phys Rev E, 64, p 051302 (2001).

**(Wolff)** Wolff and Rudd, Comp Phys Comm, 120, 200–32 (1999).

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---

## pair\_write command

### Syntax:

```
pair_write itype jtype N style inner outer file keyword Qi Qj
```

- itype,jtype = 2 atom types
- N = # of values
- style = *r* or *rsq* or *bitmap*
- inner,outer = inner and outer cutoff (distance units)
- file = name of file to write values to
- keyword = section name in file for this set of tabulated values
- Qi,Qj = 2 atom charges (charge units) (optional)

### Examples:

```
pair_write 1 3 500 r 1.0 10.0 table.txt LJ
pair_write 1 1 1000 rsq 2.0 8.0 table.txt Yukawa_1_1 -0.5 0.5
```

### Description:

Write energy and force values to a file as a function of distance for the currently defined pair potential. This is useful for plotting the potential function or otherwise debugging its values. If the file already exists, the table of values is appended to the end of the file to allow multiple tables of energy and force to be included in one file.

The energy and force values are computed at distances from inner to outer for 2 interacting atoms of type itype and jtype, using the appropriate pair\_coeff coefficients. If the style is *r*, then N distances are used, evenly spaced in *r*; if the style is *rsq*, N distances are used, evenly spaced in  $r^2$ .

For example, for N = 7, style = *r*, inner = 1.0, and outer = 4.0, values are computed at  $r = 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0$ .

If the style is *bitmap*, then  $2^N$  values are written to the file in a format and order consistent with how they are read in by the pair\_coeff command for pair style *table*. For reasonable accuracy in a bitmapped table, choose  $N \geq 12$ , an *inner* value that is smaller than the distance of closest approach of 2 atoms, and an *outer* value  $\leq$  cutoff of the potential.

If the pair potential is computed between charged atoms, the charges of the pair of interacting atoms can optionally be specified. If not specified, values of  $Q_i = Q_j = 1.0$  are used.

The file is written in the format used as input for the pair\_style table option with *keyword* as the section name. Each line written to the file lists an index number (1–N), a distance (in distance units), an energy (in energy units), and a force (in force units).

### Restrictions:

All force field coefficients for pair and other kinds of interactions must be set before this command can be invoked.

Due to how the pairwise force is computed, an inner value  $> 0.0$  must be specified even if the potential has a finite value at  $r = 0.0$ .

**Related commands:**

[pair\\_style](#), [pair\\_coeff](#)

**Default:** none

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---

## print command

**Syntax:**

```
print args
```

- args = one or more text strings and variables names to print out

**Examples:**

```
print The system volume is now $v
```

**Description:**

Print the list of arguments as a line of text to the screen and/or logfile. If variables are included in the arguments, they will be evaluated and their values printed. Note that if variables are included, the print string should not be enclosed in double quotes, else it will prevent the variables from being evaluated.

By using the print command in a section of the input script that is looped over (see the [jump](#) command), and by including variables of the *equal* style (see the [variable](#) command), a string with changing values can be printed.

**Restrictions:** none

**Related commands:**

[fix\\_print](#), [variable](#)

**Default:** none

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---

## processors command

**Syntax:**

```
processors Px Py Pz
```

- Px,Py,Pz = # of processors in each dimension of a 3d grid

**Examples:**

```
processors 2 4 4
```

**Description:**

Specify how processors are mapped as a 3d logical grid to the global simulation box.

When this command has not been specified, LAMMPS will choose Px, Py, Pz based on the dimensions of the global simulation box so as to minimize the surface/volume ratio of each processor's sub-domain.

Since LAMMPS does not load-balance by changing the grid of 3d processors on-the-fly, this command should be used to override the LAMMPS default if it is known to be sub-optimal for a particular problem. For example, a problem where the atom's extent will change dramatically over the course of the simulation.

The product of Px, Py, Pz must equal P, the total # of processors LAMMPS is running on. If multiple partitions are being used then P is the number of processors in this partition; see [this section](#) for an explanation of the `-partition` command-line switch.

If P is large and prime, a grid such as 1 x P x 1 will be required, which may incur extra communication costs.

**Restrictions:**

This command cannot be used after the simulation box is defined by a [read\\_data](#) or [create\\_box](#) command. It can be used before a restart file is read to change the 3d processor grid from what is specified in the restart file.

**Related commands:** none

**Default:**

LAMMPS chooses Px, Py, Pz

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---

## read\_data command

**Syntax:**

```
read_data file
```

- file = name of data file to read in

**Examples:**

```
read_data data.lj
read_data ../run7/data.polymer.gz
```

**Description:**



Read in a data file containing information LAMMPS needs to run a simulation. The file can be ASCII text or a gzipped text file (detected by a .gz suffix). This is one of 3 ways to specify initial atom coordinates; see the read\_restart and create\_atoms commands for alternative methods.

The structure of the data file is important, though many settings and sections are optional or can come in any order. See the examples directory for sample data files for different problems.

A data file has a header and a body. The header appears first. The first line of the header is always skipped; it typically contains a description of the file. Then lines are read one at a time. Lines can have a trailing comment starting with '#' that is ignored. If the line is blank (only whitespace after comment is deleted), it is skipped. If the line contains a header keyword, the corresponding value(s) is read from the line. If it doesn't contain a header keyword, the line begins the body of the file.

The body of the file contains zero or more sections. The first line of a section has only a keyword. The next line is skipped. The remaining lines of the section contain values. The number of lines depends on the section keyword as described below. Zero or more blank lines can be used between sections. Sections can appear in any order, with a few exceptions as noted below.

The formatting of individual lines in the data file (indentation, spacing between words and numbers) is not important except that header and section keywords (e.g. *atoms*, *xlo xhi*, *Masses*, *Bond Coeffs*) must be capitalized as shown and can't have extra white space between their words – e.g. two spaces or a tab between "Bond" and "Coeffs" is not valid.

---

These are the recognized header keywords. Header lines can come in any order. The value(s) is read from the beginning of the line. Thus the keyword *atoms* should be in a line like "1000 atoms" and the keyword *ylo yhi* should be in a line like "-10.0 10.0 ylo yhi". All these settings have a default value of 0, except the lo/hi box size defaults are -0.5 and 0.5. A line need only appear if the value is different than the default.

- *atoms* = # of atoms in system
- *bonds* = # of bonds in system
- *angles* = # of angles in system
- *dihedrals* = # of dihedrals in system
- *impropers* = # of impropers in system
- *atom types* = # of atom types in system
- *bond types* = # of bond types in system
- *angle types* = # of angle types in system
- *dihedral types* = # of dihedral types in system
- *improper types* = # of improper types in system
- *xlo xhi* = simulation box boundaries in x dimension
- *ylo yhi* = simulation box boundaries in y dimension
- *zlo zhi* = simulation box boundaries in z dimension

For 2d simulations, the *zlo zhi* values should be set to bound the z coords for atoms that appear in the file; the default of -0.5 0.5 is valid if all z coords are 0.0.

The initial simulation box size is determined by the lo/hi settings. In any dimension, the system may be periodic or non-periodic; see the boundary command.

If the system is non-periodic (in a dimension), then all atoms in the data file should have coordinates (in that dimension) between the lo and hi values. Furthermore, if running in parallel, the lo/hi values should be just a bit smaller/larger than the min/max extent of atoms. For example, if your atoms extend from 0 to 50, you

should not specify the box bounds as -10000 and 10000. Since LAMMPS uses the specified box size to layout the 3d grid of processors, this will be sub-optimal and may cause a parallel simulation to lose atoms when LAMMPS shrink-wraps the box to the atoms.

If the system is periodic (in a dimension), then atom coordinates can be outside the bounds; they will be remapped (in a periodic sense) back inside the box.

---

These are the section keywords for the body of the file.

- *Atoms, Velocities, Masses, Dipoles* = atom-property sections
- *Bonds, Angles, Dihedrals, Improvers* = molecular topology sections
- *Pair Coeffs, Bond Coeffs, Angle Coeffs, Dihedral Coeffs, Improper Coeffs* = force field sections
- *BondBond Coeffs, BondAngle Coeffs, MiddleBondTorsion Coeffs, EndBondTorsion Coeffs, AngleTorsion Coeffs, AngleAngleTorsion Coeffs, BondBond13 Coeffs, AngleAngle Coeffs* = class 2 force field sections

Each section is now listed in alphabetic order. The format of each section is described including the number of lines it must contain and rules (if any) for where it can appear in the data file.

Any individual line in the various sections can have a trailing comment starting with "#" for annotation purposes. E.g. in the Atoms section:

```
10 1 17 -1.0 10.0 5.0 6.0 # salt ion
```

---

*Angle Coeffs* section:

- one line per angle type
- line syntax: ID coeffs

```
ID = angle type (1-N)
coeffs = list of coeffs
```

- example:

```
6 70 108.5 0 0
```

The number and meaning of the coefficients are specific to the defined angle style. See the [angle style](#) and [angle coeff](#) commands for details. Coefficients can also be set via the [angle coeff](#) command in the input script.

---

*AngleAngle Coeffs* section:

- one line per improper type
- line syntax: ID coeffs

```
ID = improper type (1-N)
coeffs = list of coeffs (see improper coeff)
```

---

*AngleAngleTorsion Coeffs* section:

- one line per dihedral type
- line syntax: ID coeffs

```
ID = dihedral type (1-N)
coeffs = list of coeffs (see dihedral coeff)
```

---

*Angles* section:

- one line per angle
- line syntax: ID type atom1 atom2 atom3

```
ID = number of angle (1-Nangles)
type = angle type (1-Nangletype)
atom1,atom2,atom3 = IDs of 1st,2nd,3rd atoms in angle
```

example:

```
2 2 17 29 430
```

The 3 atoms are ordered linearly within the angle. E.g H,O,H for a water molecule. The *Angles* section must appear after the *Atoms* section. All values in this section must be integers (1, not 1.0).

---

*AngleTorsion Coeffs* section:

- one line per dihedral type
- line syntax: ID coeffs

```
ID = dihedral type (1-N)
coeffs = list of coeffs (see dihedral coeff)
```

---

*Atoms* section:

- one line per atom
- line syntax: depends on atom style

This is the list of all possible quantities that can appear on each line of this section:

- atom-ID = integer ID of atom
- molecule-ID = integer ID of molecule the atom belongs to
- type-ID = integer type ID of atom (1-Ntype)
- q = charge on atom
- diameter = diameter of atom
- density = density of atom
- x,y,z = coordinates of atom
- mux,muy,muz = components of dipole orientation of atom
- nx,ny,nz = image indices for atom

Which of these quantities are actually listed depends on the [atom style](#). This is the list of which styles require each quantity:

- atom-ID = all styles
- molecule-ID = angle, bond, molecular, full styles
- type-ID = all styles
- q = charge, dipole, full styles
- diameter = granular style

- density = granular style
- x,y,z = all styles
- mux,muy,muz = dipole style
- nx,ny,nz = optional for all styles (see below)

Any quantity that is used by the atom style appears in the order listed above. Thus if the atom style is *atomic*, an atom line should have 5 quantities: atom-ID, type-ID, x, y, z. If the atom style is *hybrid eam dipole molecular*, then an atom line should have 10 quantities: atom-ID, molecule-ID, type-ID, q, x, y, z, mux, muy, muz.

The units for these quantities depend on the unit style; see the units command for details.

For 2d simulations specify z as 0.0, or whatever value is within the *zlo zhi* setting in the data file header.

The atom-ID is used to identify the atom throughout the simulation and in dump files. Normally, it is a unique value from 1 to Natoms for each atom. Unique values larger than Natoms can be used, but they will cause extra memory to be allocated on each processor, if an atom map array is used (see the atom\_modify command). If an atom map array is not used (e.g. an atomic system with no bonds), velocities are not assigned in the data file, and you don't care if unique atom IDs appear in dump files, then IDs can be set to non-unique values > 0.

The molecule ID is a 2nd identifier attached to an atom. Normally, it is a number from 1 to N, identifying which molecule the atom belongs to. It can be 0 if it is an unbonded atom or if you don't care about molecule assignments.

An *Atoms* section must appear in the data file if natoms > 0 in the header section. The atoms can be listed in any order.

Atom lines (all or none of them) can optionally list 3 final integer values: nx,ny,nz. For periodic dimensions, they specify which image of the box the atom is considered to be in. An image of 0 means the box as defined. A value of 2 means add 2 box lengths to get the true value. A value of -1 means subtract 1 box length to get the true value. LAMMPS updates these flags as atoms cross periodic boundaries during the simulation. The flags can be output via the dump and dump\_modify commands. If nx,ny,nz values are not set in the data file, LAMMPS initializes them to 0.

Atom velocities are set to 0.0 when the *Atoms* section is read. They may later be set by a *Velocities* section or by a velocity command in the input script.

*Bond Coeffs* section:

- one line per bond type
- line syntax: ID coeffs

```
ID = bond type (1-N)
coeffs = list of coeffs
```

- example:

```
4 250 1.49
```

The number and meaning of the coefficients are specific to the defined bond style. See the bond\_style and bond\_coeff commands for details. Coefficients can also be set via the bond\_coeff command in the input

script.

---

*BondAngle Coeffs* section:

- one line per angle type
- line syntax: ID coeffs

```
ID = angle type (1-N)
coeffs = list of coeffs (see class 2 section of angle coeff)
```

---

*BondBond Coeffs* section:

- one line per angle type
- line syntax: ID coeffs

```
ID = angle type (1-N)
coeffs = list of coeffs (see class 2 section of angle coeff)
```

---

*BondBond13 Coeffs* section:

- one line per dihedral type
- line syntax: ID coeffs

```
ID = dihedral type (1-N)
coeffs = list of coeffs (see class 2 section of dihedral coeff)
```

---

*Bonds* section:

- one line per bond
- line syntax: ID type atom1 atom2

```
ID = bond number (1-Nbonds)
type = bond type (1-Nbondtype)
atom1,atom2 = IDs of 1st,2nd atoms in bond
```

- example:

```
12 3 17 29
```

The *Bonds* section must appear after the *Atoms* section. All values in this section must be integers (1, not 1.0).

---

*Dihedral Coeffs* section:

- one line per dihedral type
- line syntax: ID coeffs

```
ID = dihedral type (1-N)
coeffs = list of coeffs
```

- example:

```
3 0.6 1 0 1
```

The number and meaning of the coefficients are specific to the defined dihedral style. See the [dihedral style](#)

and [dihedral coeff](#) commands for details. Coefficients can also be set via the [dihedral coeff](#) command in the input script.

---

*Dihedrals* section:

- one line per dihedral
- line syntax: ID type atom1 atom2 atom3 atom4

```
ID = number of dihedral (1-Ndihedrals)
type = dihedral type (1-Ndihedraltype)
atom1,atom2,atom3,atom4 = IDs of 1st,2nd,3rd,4th atoms in dihedral
```

- example:

```
12 4 17 29 30 21
```

The 4 atoms are ordered linearly within the dihedral. The *Dihedrals* section must appear after the *Atoms* section. All values in this section must be integers (1, not 1.0).

---

*Dipoles* section:

- one line per atom type line syntax: ID dipole-moment

```
ID = atom type (1-N)
dipole-moment = value of dipole moment
```

- example:

```
2 0.5
```

This defines the dipole moment of each atom type (which can be 0.0 for some types). This can also be set via the [dipole](#) command in the input script.

---

*EndBondTorsion Coeffs* section:

- one line per dihedral type
- line syntax: ID coeffs

```
ID = dihedral type (1-N)
coeffs = list of coeffs (see class 2 section of dihedral coeff)
```

---

*Improper Coeffs* section:

- one line per improper type
- line syntax: ID coeffs

```
ID = improper type (1-N)
coeffs = list of coeffs
```

- example:

```
2 20 0.0548311
```

The number and meaning of the coefficients are specific to the defined improper style. See the [improper style](#) and [improper coeff](#) commands for details. Coefficients can also be set via the [improper coeff](#) command in

the input script.

---

*Impropers* section:

- one line per improper
- line syntax: ID type atom1 atom2 atom3 atom4

```
ID = number of improper (1-Nimpropers)
type = improper type (1-Nimproptype)
atom1,atom2,atom3,atom4 = IDs of 1st,2nd,3rd,4th atoms in improper
```

- example:

```
12 3 17 29 13 100
```

The *Impropers* section must appear after the *Atoms* section. All values in this section must be integers (1, not 1.0).

---

*Masses* section:

- one line per atom type
- line syntax: ID mass

```
ID = atom type (1-N)
mass = mass value
```

- example:

```
3 1.01
```

This defines the mass of each atom type. This can also be set via the mass command in the input script. This section should not be used for atom styles that define a mass for individual atoms – e.g. atom style granular.

---

*MiddleBondTorsion Coeffs* section:

- one line per dihedral type
- line syntax: ID coeffs

```
ID = dihedral type (1-N)
coeffs = list of coeffs (see class 2 section of dihedral coeff)
```

---

*Pair Coeffs* section:

- one line per atom type
- line syntax: ID coeffs

```
ID = atom type (1-N)
coeffs = list of coeffs
```

- example:

```
3 0.022 2.35197 0.022 2.35197
```

The number and meaning of the coefficients are specific to the defined pair style. See the pair\_style and pair\_coeff commands for details. Coefficients can also be set via the pair\_coeff command in the input script.

---

*Velocities* section:

one line per atom

- line syntax: atom-ID vx vy vz

atom-ID = integer ID of atom to assign velocity to

vx,vy,vz = components of velocity of the atom

- example:

```
45 -3.4 0.05 1.25
```

The velocity lines can appear in any order. This section can only be used after an *Atoms* section. The *Atoms* section must have assigned a unique atom ID to each atom so that velocities can be assigned in this way. Velocities can also be set by the [velocity](#) command in the input script.

---

### Restrictions:

To read gzipped data files, you must compile LAMMPS with the `-DGZIP` option – see the [Making LAMMPS](#) section of the documentation.

### Related commands:

[read\\_restart](#), [create\\_atoms](#)

**Default:** none

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---

## read\_restart command

### Syntax:

```
read_restart file
```

- file = name of binary restart file to read in

### Examples:

```
read_restart save.10000
```

### Description:

Read in a previously saved problem from a restart file. This allows continuation of a previous run.

Restart files are saved in binary format to enable exact restarts, meaning that the trajectories of a restarted run will precisely match those produced by the original run had it continued on. Several things can prevent exact restarts due to round-off effects, in which case the trajectories in the 2 runs will slowly diverge. These include running on a different number of processors or changing certain settings such as those set by the [newton](#) or [processors](#) commands. LAMMPS will issue a WARNING in these cases. Certain fixes will also not restart exactly, though they should provide statistically similar results. These include the shake and langevin styles. If



a restarted run is immediately different than the run which produced the restart file, it could be a LAMMPS bug, so consider reporting it if you think the behavior is wrong.

Because restart files are binary, they may not be portable to other machines. They can be converted to ASCII data files using the `restart2data` tool in the `tools` sub-directory of the LAMMPS distribution.

A restart file stores the units and atom style, simulation box attributes, individual atoms and their attributes including molecular topology, force field styles and coefficients, special\_bonds settings, and atom group definitions. This means that commands for these quantities do not need to be specified in your input script that reads the restart file. The exceptions to this are listed below in the Restrictions section.

Information about the kspace\_style settings are not stored in the restart file. Hence if you wish to invoke an Ewald or PPPM solver, this command must be re-issued after the restart file is read.

The restart file also stores values for any fixes that require state information to enable restarting where they left off. These include the *nvt* and *npt* styles that have a global state, as well as the *msd* and *wall/gran* styles that store information about each atom.

Fix commands are not stored in the restart file which means they must be specified in the input script that reads the restart file. To re-enable a fix whose state was stored in the restart file, the fix command in the new input script must use the same fix-ID and group-ID as the input script that wrote the restart file. LAMMPS will print a message indicating that the fix is being re-enabled.

Note that no other information is stored in the restart file. This means that your new input script should specify settings for quantities like timestep size, thermodynamic and dump output, etc.

Bond interactions (angle, etc) that have been turned off by the fix shake or delete\_bonds command will be written to a restart file as if they are turned on. This means they will need to be turned off again in a new run after the restart file is read.

Bonds that are broken (e.g. by a bond-breaking potential) are written to the restart file as broken bonds with a type of 0. Thus these bonds will still be broken when the restart file is read.

### Restrictions:

The pair\_style *eam*, *table*, and *hybrid* styles do not store coefficient data for individual atom type pairs in the restart file. Nor does the bond\_style *hybrid* style. Thus you must use new pair\_coeff and bond\_coeff commands to read the appropriate tabulated files or reset the coefficients after the restart file is read.

### Related commands:

read\_data, write\_restart, restart

**Default:** none

---

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---

## region command

### Syntax:

region ID style args keyword value ...

- ID = user-assigned name for the region
- style = *block* or *sphere* or *cylinder* or *union* or *intersect*

```
block args = xlo xhi ylo yhi zlo zhi
             xlo,xhi,ylo,yhi,zlo,zhi = bounds of block in all
             dimensions (distance units)
sphere args = x y z radius
             x,y,z = center of sphere (distance units)
             radius = radius of sphere (distance units)
cylinder args = dim c1 c2 radius lo hi
             dim = x or y or z = axis of cylinder
             c1,c2 = coords of cylinder axis in other 2 dimensions (distance units)
             radius = cylinder radius (distance units)
             lo,hi = bounds of cylinder in dim (distance units)
union args = N reg-ID1 reg-ID2 ...
             N = # of regions to follow, must be 2 or greater
             reg-ID1,reg-ID2, ... = IDs of regions to join together
intersect args = N reg-ID1 reg-ID2 ...
             N = # of regions to follow, must be 2 or greater
             reg-ID1,reg-ID2, ... = IDs of regions to intersect
```

- zero or more keyword/value pairs may be appended to the args
- keyword = *side* or *units*

```
side value = in or out
             in = the region is inside the specified geometry
             out = the region is outside the specified geometry
units value = lattice or box
             lattice = the geometry is defined in lattice units
             box = the geometry is defined in simulation box units
```

### Examples:

```
region 1 block -3.0 5.0 INF 10.0 INF INF
region 2 sphere 0.0 0.0 0.0 5 side out
region void cylinder y 2 3 5 -5.0 INF units box
region outside union 4 side1 side2 side3 side4
```

### Description:

This command defines a geometric region of space. Various other commands use regions. For example, the region can be filled with atoms via the create\_atoms command. Or the atoms in the region can be identified as a group via the group command, or deleted via the delete\_atoms command.

The lo/hi values for *block* or *cylinder* styles can be specified as INF which means they extend all the way to the global simulation box boundary. If a region is defined before the simulation box has been created (via create\_box or read\_data or read\_restart commands), then an INF parameter cannot be used.

For style *cylinder*, the c1,c2 params are coordinates in the 2 other dimensions besides the cylinder axis dimension. For dim = x, c1/c2 = y/z; for dim = y, c1/c2 = x/z; for dim = z, c1/c2 = x/y. Thus the third example above specifies a cylinder with its axis in the y-direction located at x = 2.0 and z = 3.0, with a radius of 5.0,

and extending in the y-direction from -5.0 to the upper box boundary.

The *union* style creates a region consisting of the volume of all the listed regions combined. The *inteseect* style creates a region consisting of the volume that is common to all the listed regions.

The *side* keyword determines whether the region is considered to be inside or outside of the specified geometry. Using this keyword in conjunction with *union* and *intersect* regions, complex geometries can be built up. For example, if the interior of two spheres were each defined as regions, and a *union* style with *side* = out was constructed listing the region-IDs of the 2 spheres, the resulting region would be all the volume in the simulation box that was outside both of the spheres.

The *units* keyword determines the meaning of the distance units used to define the region. A *box* value selects standard distance units as defined by the units command, e.g. Angstroms for units = real or metal. A *lattice* value means the distance units are in cubic lattice spacings. The lattice command must first be used to define a lattice.

**Restrictions:** none

**Related commands:**

lattice, create\_atoms, delete\_atoms, group

**Default:**

The option defaults are side = in and units = lattice.

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---

## replicate command

**Syntax:**

```
replicate nx ny nz
```

- nx,ny,nz = replication factors in each dimension

**Examples:**

```
replicate 2 3 2
```

**Description:**

Replicate the current simulation one or more times in each dimension. For example, replication factors of 2,2,2 will create a simulation with 8x as many atoms by doubling the simulation domain in each dimension. A replication factor of 1 in a dimension leaves the simulation domain unchanged.

All properties of the atoms are replicated, including their velocities, which may or may not be desirable. New atom IDs (tags) are assigned to new atoms, as are molecule IDs. Bonds and other topology interactions are created between pairs of new atoms as well as between old and new atoms. This is done by using the image flag for each atom to "unwrap" it out of the periodic box before replicating it. This means that molecular bonds you specify in the original data file that span the periodic box should be between two atoms with image

flags that differ by 1. This will allow them to be unwrapped appropriately.

This command operates similar to the replicate tool in the tools sub-directory of the LAMMPS distribution which creates new data files from old ones.

**Restrictions:**

A 2d simulation cannot be replicated in the z dimension.

If a simulation is non-periodic in a dimension, care should be used when replicating it in that dimension, as it may put atoms nearly on top of each other.

If the current simulation was read in from a restart file (before a run is performed), there can have been no fix information stored in the file for individual atoms. Similarly, no fixes can be defined at the time the replicate command is used that require vectors of atom information to be stored. This is because the replicate command does not know how to replicate that information for new atoms it creates.

**Related commands:** none

**Default:** none

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---

## reset\_timestep command

**Syntax:**

```
reset_timestep N
```

- N = timestep number

**Examples:**

```
reset_timestep 0  
reset_timestep 4000000
```

**Description:**

Set the timestep counter to the specified value. This command normally comes after the timestep has been set by reading it in from a file or a previous simulation advanced the timestep.

The [read\\_data](#) and [create\\_box](#) commands set the timestep to 0; the [read\\_restart](#) command sets the timestep to the value it had when the restart file was written.

**Restrictions:** none

**Related commands:** none

**Default:** none

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---

## restart command

### Syntax:

```
restart 0
restart N root
restart N file1 file2
```

- N = write a restart file every this many timesteps
- root = filename to which timestep # is appended
- file1,file2 = two full filenames, toggle between them when writing file

### Examples:

```
restart 0
restart 1000 poly.restart
restart 10000 poly.r.1 poly.r.2
```

### Description:

Write out a binary restart file every so many timesteps as a run proceeds. A value of 0 means do not write out restart files. Using one filename as an argument will create a series of filenames with a timestep suffix, e.g. the 2nd example above will create poly.restart.1000, poly.restart.2000, poly.restart.3000, etc. Using two filenames will produce only 2 restart files. LAMMPS will toggle between the 2 names as it writes successive restart files.

Restart files are written on timesteps that are a multiple of N and on the last timestep of a simulation.

See the [read\\_restart](#) command for information about what is stored in a restart file.

Restart files can be read by a [read\\_restart](#) command to restart a simulation from a particular state. Because the file is binary (to enable exact restarts), it may not be readable on another machine. In this case, the [restart2data program](#) in the tools directory can be used to convert a restart file to an ASCII data file.

**Restrictions:** none

### Related commands:

[write\\_restart](#), [read\\_restart](#)

### Default:

```
restart 0
```

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---

## run command

### Syntax:

```
run N
```

- N = # of timesteps

### Examples:

```
run 10000
```

### Description:

Run or continue dynamics for the specified number of timesteps.

When the run style is *respa*, N refers to outer loop (largest) timesteps.

A value of N = 0 is acceptable; only the thermodynamics of the system are computed and printed without taking a timestep.

**Restrictions:** none

**Related commands:**

[minimize](#), [run\\_style](#), [temper](#)

**Default:** none

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---

## run\_style command

### Syntax:

```
run_style style args
```

- style = *verlet* or *respa*

```
verlet args = none
```

```
respa args = N n1 n2 ... keyword values ...
```

N = # of levels of rRESPA

n1, n2, ... = loop factor between rRESPA levels (N-1 values)

zero or more keyword/value pairings may be appended to the loop factors

keyword = *bond* or *angle* or *dihedral* or *improper* or

*pair* or *inner* or *middle* or *outer* or *kspace*

*bond* value = M

M = which level (1-N) to compute bond forces in

*angle* value = M

M = which level (1-N) to compute angle forces in

*dihedral* value = M

M = which level (1-N) to compute dihedral forces in

*improper* value = M

```

    M = which level (1-N) to compute improper forces in
pair value = M
    M = which level (1-N) to compute pair forces in
inner values = M cut1 cut2
    M = which level (1-N) to compute pair inner forces in
    cut1 = inner cutoff between pair inner and
           pair middle or outer (distance units)
    cut2 = outer cutoff between pair inner and
           pair middle or outer (distance units)
middle values = M cut1 cut2
    M = which level (1-N) to compute pair middle forces in
    cut1 = inner cutoff between pair middle and pair outer (distance units)
    cut2 = outer cutoff between pair middle and pair outer (distance units)
outer value = M
    M = which level (1-N) to compute pair outer forces in
kspace value = M
    M = which level (1-N) to compute kspace forces in

```

### Examples:

```

run_style verlet
run_style respa 4 2 2 2 bond 1 dihedral 2 pair 3 kspace 4
run_style respa 4 2 2 2 bond 1 dihedral 2 inner 3 5.0 6.0 outer 4 kspace 4

```

### Description:

Choose the style of time integrator used for molecular dynamics simulations performed by LAMMPS.

The *verlet* style is a velocity–Verlet integrator.

The *respa* style implements the rRESPA multi–timescale integrator ([Tuckerman](#)) with N hierarchical levels, where level 1 is the innermost loop (shortest timestep) and level N is the outermost loop (largest timestep). The loop factor arguments specify what the looping factor is between levels. N1 specifies the number of iterations of level 1 for a single iteration of level 2, N2 is the iterations of level 2 per iteration of level 3, etc. N–1 looping parameters must be specified.

The timestep command sets the timestep for the outermost rRESPA level. Thus if the example command above for a 4–level rRESPA had an outer timestep of 4.0 fmsec, the inner timestep would be 8x smaller or 0.5 fmsec. All other LAMMPS commands that specify number of timesteps (e.g. neigh\_modify parameters, dump every N timesteps, etc) refer to the outermost timesteps.

The rRESPA keywords enable you to specify at what level of the hierarchy various forces will be computed. If not specified, the defaults are that bond forces are computed at level 1 (innermost loop), angle forces are computed where bond forces are, dihedral forces are computed where angle forces are, improper forces are computed where dihedral forces are, pair forces are computed at the outermost level, and kspace forces are computed where pair forces are. The inner, middle, outer forces have no defaults.

The *inner* and *middle* keywords take additional arguments for cutoffs that are used by the force computations. If the 2 cutoffs for *inner* are 5.0 and 6.0, this means that all pairs up to 6.0 apart are computed by the inner force. Those between 5.0 and 6.0 have their force go ramped to 0.0 so the overlap with the next regime (middle or outer) is smooth. The next regime (middle or outer) will compute forces for all pairs from 5.0 outward, with those from 5.0 to 6.0 having their value ramped in an inverse manner.

When using rRESPA (or for any MD simulation) care must be taken to choose a timestep size(s) that insures

the Hamiltonian for the chosen ensemble is conserved. For the constant NVE ensemble, total energy must be conserved. Unfortunately, it is difficult to know *a priori* how well energy will be conserved, and a fairly long test simulation (~10 ps) is usually necessary in order to verify that no long-term drift in energy occurs with the trial set of parameters.

With that caveat, a few rules-of-thumb may be useful in selecting *respa* settings. The following applies mostly to biomolecular simulations using the CHARMM or a similar all-atom force field, but the concepts are adaptable to other problems. Without SHAKE, bonds involving hydrogen atoms exhibit high-frequency vibrations and require a timestep on the order of 0.5 fmsec in order to conserve energy. The relatively inexpensive force computations for the bonds, angles, impropers, and dihedrals can be computed on this innermost 0.5 fmsec step. The outermost timestep cannot be greater than 4.0 fmsec without risking energy drift. Smooth switching of forces between the levels of the rRESPA hierarchy is also necessary to avoid drift, and a 1–2 angstrom "healing distance" (the distance between the outer and inner cutoffs) works reasonably well. We thus recommend the following settings for use of the *respa* style without SHAKE in biomolecular simulations:

```
timestep 4.0
run_style respa 4 2 2 2 inner 2 4.5 6.0 middle 3 8.0 10.0 outer 4
```

With these settings, users can expect good energy conservation and roughly a 2.5 fold speedup over the *verlet* style with a 0.5 fmsec timestep.

If SHAKE is used with the *respa* style, time reversibility is lost, but substantially longer time steps can be achieved. For biomolecular simulations using the CHARMM or similar all-atom force field, bonds involving hydrogen atoms exhibit high frequency vibrations and require a time step on the order of 0.5 fmsec in order to conserve energy. These high frequency modes also limit the outer time step sizes since the modes are coupled. It is therefore desirable to use SHAKE with *respa* in order to freeze out these high frequency motions and increase the size of the time steps in the *respa* hierarchy. The following settings can be used for biomolecular simulations with SHAKE and rRESPA:

```
fix 2 all shake 0.000001 500 0 m 1.0 a 1
timestep 4.0
run_style respa 2 2 inner 1 4.0 5.0 outer 2
```

With these settings, users can expect good energy conservation and roughly a 1.5 fold speedup over the *verlet* style with SHAKE and a 2.0 fmsec timestep.

For non-biomolecular simulations, the *respa* style can be advantageous if there is a clear separation of time scales – fast and slow modes in the simulation. Even a LJ system can benefit from rRESPA if the interactions are divided by the inner, middle and outer keywords. A 2-fold or more speedup can be obtained while maintaining good energy conservation. In real units, for a pure LJ fluid at liquid density, with a sigma of 3.0 angstroms, and epsilon of 0.1 Kcal/mol, the following settings seem to work well:

```
timestep 36.0
run_style respa 3 3 4 inner 1 3.0 4.0 middle 2 6.0 7.0 outer 3
```

**Restrictions:** none

Whenever using rRESPA, the user should experiment with trade-offs in speed and accuracy for their system, and verify that they are conserving energy to adequate precision.

**Related commands:**

run command



[timestep, run](#)

### Default:

```
run_style verlet
```

---

(**Tuckerman**) Tuckerman, Berne and Martyna, J Chem Phys, 97, p 1990 (1992).

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## set command

### Syntax:

```
set group-ID style value
```

- group-ID = ID of group
- style = *atom* or *bond* or *angle* or *dihedral* or *improper* or *charge* or *dipole*
- value = value to set selected atoms to

### Examples:

```
set solvent atom 2
set edge bond 4
set half charge 0.5
```

### Description:

Set an attribute for atoms in the group. Since these attributes are assigned by the [read\\_data](#), [read\\_restart](#) or [create\\_atoms](#) commands, this command changes those assignments. This can be useful for altering pairwise and molecular force interactions, since force-field coefficients are defined in terms of types. It can also be used to change the labeling of atoms when they are output in [dump](#) files.

For style *atom*, the atom type of all atoms in the group is changed to the specified value from 1 to ntypes. Note that ntypes must be within the range the simulation was initialized for. The maximum number of types is set by the [create\\_box](#) command or the *atom types* field in the header of the data file read by the [read\\_data](#) command.

For style *bond*, *angle*, *dihedral*, or *improper*, the bond type (angle type, etc) of all bonds (angles, etc) of atoms in the group is changed to the specified value from 1 to nbondtypes (angletypes, etc). All atoms in the bond (angle, etc) must be in the group in order for the change to be made. The maximum number of types is set by the *bond types* (*angle types*, etc) field in the header of the data file.

For style *charge*, the charge of each atom in the group is set to the specified value.

For style *dipole*, the specified value is used as a random number seed. The dipole moment of each atom in the group is set to a random orientation with a magnitude determined by the [dipole](#) command setting for that atom type.

### Restrictions:

set command

This command requires inter-processor communication to coordinate the setting of bond types (angle types, etc). This means that your system must be ready to perform a simulation before using this command (force fields setup, atom masses set, etc). This is not necessary to simply reset atom types.

#### Related commands:

[create\\_box](#), [create\\_atoms](#), [read\\_data](#)

**Default:** none

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## special\_bonds command

### Syntax:

```
special_bonds style
special_bonds c1 c2 c3
special_bonds c1 c2 c3 c4 c5 c6
```

- style = *charmm* or *amber*
- c1,c2,c3,c4,c5,c6 = numeric coefficients from 0.0 to 1.0

### Examples:

```
special_bonds charmm
special_bonds amber
special_bonds 0.0 0.0 1.0
special_bonds 0.0 0.0 1.0 0.0 0.0 0.5
```

### Description:

Set the weighting coefficients for the pairwise force and energy contributions from atom pairs that are also bonded to each other directly or indirectly. The 1st coefficient is the weighting factor on 1–2 atom pairs, which are those directly bonded to each other. The 2nd coefficient is the weighting factor on 1–3 atom pairs which are those separated by 2 bonds (e.g. the 2 H atoms in a water molecule). The 3rd coefficient is the weighting factor on 1–4 atom pairs which are separated by 3 bonds (e.g. the 1st and 4th atoms in a dihedral interaction).

Note that for purposes of computing weighted pairwise interactions, 1–3 and 1–4 interactions are not defined from the list of angles or dihedrals used by the simulation. Rather, they are inferred topologically by the set of bonds defined when atoms are read in from a file ([read\\_data](#) or [read\\_restart](#)). Thus the set of 1–2,1–3,1–4 interactions is the same whether angle potentials are computed or not, and remains the same even if bonds are constrained, or turned off, or removed during a simulation. The only exception is if the [delete\\_bonds](#) command is used with the *special* option that recomputes the 1–2,1–3,1–4 topologies; see the command for more details.

The *charmm* style sets all 3 coefficients to 0.0, which is the default for the CHARMM force field. In pair styles *lj/charmm/coul/charmm* and *lj/charmm/coul/long* the 1–4 coefficients are defined explicitly, and these pair-wise contributions are computed in the charmm dihedral style – see the [pair\\_coeff](#) and [dihedral\\_style](#) commands for more information.

The *amber* style sets the 3 coefficients to 0.0 0.0 0.5 for LJ interactions and to 0.0 0.0 0.833 for Coulombic interactions, which is the default for a particular version of the AMBER force field, where the last value is 5/6.

A `special_bonds` command with 3 coefficients sets the 1–2, 1–3, and 1–4 coefficients for both LJ and Coulombic terms to those values.

A `special_bonds` command with 6 coefficients sets the 1–2, 1–3, and 1–4 LJ coefficients to the first 3 values and the Coulombic coefficients to the last 3 values.

**Restrictions:** none

**Related commands:**

[delete\\_bonds](#)

**Default:**

```
special_bonds 0.0 0.0 0.0
```

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---

## temp\_modify command

**Syntax:**

```
temp_modify temp-ID keyword value ...
```

- temp-ID = ID of temperature to modify
- one or more keyword/value pairs may be listed
- keyword = *extra*

```
extra value = N
```

```
N = # of extra degrees of freedom to subtract
```

**Examples:**

```
temp_modify mine extra 0
```

**Description:**

Modify the parameters of a previously defined temperature method. This can either be the default temperature defined by LAMMPS (ID = *default*) or a user-defined temperature created by using the [temperature](#) command.

The *extra* keyword refers to how many degrees-of-freedom are subtracted (typically from 3N) as a normalizing factor in the temperature computation. The default is 3 which is a correction factor for an ensemble of velocities with zero total linear momentum.

**Restrictions:** none

## Related commands:

[temperature](#)

## Default:

The option defaults are `extra = 3`.

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## temper command

### Syntax:

```
temper N M temp fix-ID seed1 seed2 index
```

- `N` = total # of timesteps to run
- `M` = attempt a tempering swap every this many steps
- `temp` = initial temperature for this ensemble
- `fix-ID` = ID of the fix that will control temperature during the run
- `seed1` = random # seed used to decide on adjacent temperature to partner with
- `seed2` = random # seed for Boltzmann factor in Metropolis swap
- `index` = which temperature (0 to `N-1`) I am simulating (optional)

### Examples:

```
temper 100000 100 $t tempfix 0 58728
temper 40000 100 $t tempfix 0 32285 $w
```

### Description:

Run a parallel tempering (replica exchange) simulation of multiple ensembles of a system on multiple partitions of processors. The processor partitions are defined using the `-partition` command-line switch (see [this section](#)). Each ensemble's temperature is typically controlled at a different value by a fix with ID `fix-ID` that controls temperature. Possible fix styles are [nvt](#), [npt](#), and [temp/rescale](#). The desired temperature is specified by `temp`, which is typically a variable previously set in the input script, so that each partition is assigned a different temperature. See the [variable](#) command for more details. For example,

```
variable t world 300.0 310.0 320.0 330.0
```

As the tempering simulation runs for `N` timesteps, a swap between adjacent ensembles will be attempted every `M` timesteps. If `seed1` is 0, then the swap attempts will alternate between odd and even pairings. If `seed1` is non-zero then it is used as a seed in a random number generator to randomly choose an odd or even pairing each time. Each attempted swap of temperatures is either accepted or rejected based on a Boltzmann-weighted Metropolis criterion which uses `seed2` in the random number generator.

The last argument `index` is optional and is used when restarting a tempering run from a set of restart files (one for each replica) which had previously swapped to new temperatures. The `index` value (from 0 to `N-1`, where `N` is the # of replicas) identifies which temperature the replica was simulating on the timestep the restart files were written. Obviously, this argument must be a variable so that each partition has the correct value. Set the variable to the `N` values listed in the log file for the previous run for the replica temperatures at that timestep.

For example if the log file listed

```
500000 2 4 0 1 3
```

then a setting of

```
variable w proc 2 4 0 1 3
```

would be used to restart the run with a tempering command like the example above with \$w as the last argument.

**Restrictions:** none

**Related commands:**

[variable](#)

**Default:** none

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## temperature command

**Syntax:**

```
temperature ID group-ID style args keyword value ...
```

- ID = user-assigned name for the temperature
- group-ID = ID of group of atoms to compute the temperature for
- style = *full* or *partial* or *ramp* or *region*

```
full args = none
partial args = x y z
             x,y,z = 0 or 1
ramp args = vdim vlo vhi dim clo chi
             vdim = vx or vy or vz
             vlo,vhi = subtract velocities between vlo and vhi (velocity units)
             dim = x or y or z
             clo,chi = lower and upper bound of domain to
                       subtract from (distance units)
region args = region-ID
             region-ID = ID of region to use for choosing atoms
```

- zero or more keyword/value pairs may be appended to the args
- keyword = *units*

```
units value = lattice or box
```

**Examples:**

```
temperature mine peptide full
temperature new flow partial 1 1 0
temperature mine flow region boundary
temperature 2nd middle ramp vx 0 8 y 2 12 units lattice
```

## Description:

Define a method for computing the temperature of a group of atoms.

The ID of the temperature can be referred to in other commands, such as thermo\_modify, velocity, fix\_modify, temp\_modify. Note that certain fixes create their own temperatures with the same ID as the fix, e.g. fix temp/rescale, fix nvt, fix npt, etc.

The style determines how the temperature is computed. The *full* style means  $KE = \text{dim}/2 N k T$ , where KE = total kinetic energy of the group of atoms (sum of  $1/2 m v^2$ ), dim = 2 or 3 = dimensionality of the simulation, N = number of atoms in the group, k = Boltzmann constant, and T = temperature.

The *partial* style uses the same formula as *full*, except entire dimensions can be eliminated from the kinetic energy computation. This can be useful for systems where atoms are flowing, and only the thermal temperature in the non-flow directions is desired. A "0" means do not use the component of velocity in that dimension when computing KE. In the example above with arguments 1 1 0, only x and y velocities (not z) would be used in computing KE and temperature.

The *ramp* style can be used to eliminate an imposed velocity on a system before computing thermal KE. The meaning of these arguments is the same as for the velocity command which was presumably used to impose the velocity.

The *region* style is the same as *full* except that only atoms in the specified geometric region contribute to the temperature. Since atoms can enter/leave a region, this test is performed each time the temperature is computed. This can be useful for thermostating one portion of the simulation box. E.g. a McDLT simulation where one side is cooled, and the other side is heated.

Note that a *region*-style temperature can be used to thermostat with fix temp/rescale or fix langevin, but should probably not be used with Nose/Hoover style fixes (>fix nvt, fix npt, or fix nph), if the degrees-of-freedom included in the computed T varies with time.

The *units* keyword determines the meaning of the distance units used for coordinates (c1,c2) and velocities (vlo,vhi) defined for the *ramp* style. A *box* value selects standard distance units as defined by the units command, e.g. Angstroms for units = real or metal. A *lattice* value means the distance units are in cubic lattice spacings; e.g. lattice spacings / tau. The lattice command must first be used to define a lattice.

LAMMPS defines a temperature with ID = *default* which computes a *full* style on the *all* group of atoms. This is the temperature used for thermodynamic output of quantities like temperature, pressure, kinetic energy (see the thermo\_style command) unless you change it via the thermo\_modify command.

All temperature styles (except *region*) subtract out degrees-of-freedom (DOF) due to fixes that constrain molecular motion. Currently, these are fix shake and fix rigid. DOF is the  $N * \text{dim}$  factor in the above equation for the *full* style. This means the temperature of groups of atoms that include these constraints will be computed correctly. If needed, the subtracted degrees-of-freedom can be tweaked using the temp\_modify command.

**Restrictions:** none

**Related commands:**

thermo\_modify, velocity, fix\_modify, temp\_modify

**Default:**

A temperature with ID = *default* is defined by LAMMPS, as if it had been specified as "temperature default all full". The option default is units = lattice.

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## thermo command

**Syntax:**

```
thermo N
```

- N = output thermodynamics every N timesteps

**Examples:**

```
thermo 100
```

**Description:**

Compute and print thermodynamics (temperature, energy, pressure) on timesteps that are a multiple of N. A value of 0 will only compute and print thermodynamics at the beginning and end of a simulation.

**Restrictions:** none

**Related commands:**

[thermo\\_style](#), [thermo\\_modify](#)

**Default:**

```
thermo 0
```

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---

## thermo\_modify command

**Syntax:**

```
thermo_modify keyword value ...
```

- one or more keyword/value pairs may be listed
- keyword = *temp* or *lost* or *norm* or *flush* or *line* or *format*

```
temp value = ID of temperature
lost value = error or warn or ignore
norm value = yes or no
flush value = yes or no
line value = one or multi
format value = int string or float string or N string
N = integer from 1 to # of quantities being printed
```

```

    string = C-style format string
    window value = N
    N = number of previous print-outs to average over

```

### Examples:

```

thermo_modify temp mydef
thermo_modify lost no flush yes
thermo_modify line multi format float %g format 3 %15.8g

```

### Description:

Set options for how thermodynamics are computed and printed by LAMMPS.

The *temp* option allows you to specify how temperature is computed when used to output thermodynamic info (temperature, kinetic energy, pressure). Different methods of computing temperature can be defined via the temperature command.

The *lost* option determines whether LAMMPS checks for lost atoms each time it computes thermodynamics and what it does if atoms are lost. If the value is *ignore*, LAMMPS does not check for lost atoms. If the value is *error* or *warn*, LAMMPS checks and either issues an error or warning. The code will exit with an error and continue with a warning. This can be a useful debugging option.

The *norm* option determines whether the thermodynamic print-out is normalized by the number of atoms or is the total summed across all atoms. Different unit styles have different defaults for this setting.

The *flush* option invokes a flush operation after thermodynamic info is written to the log file. This insures the output in that file is current (no buffering by the OS), even if LAMMPS halts before the simulation completes.

The *line* option determines whether thermodynamics will be printed as a series of numeric values on one line or in a multi-line format with 3 quantities with text strings per line and a dashed-line header containing the timestep and CPU time. This modify option overrides the *one* and *multi* thermo\_style settings.

The *format* option sets the numeric format of individual printed quantities. The *int* and *float* settings set the format for all integer or floating-point quantities printed. The setting with a numeric value (e.g. format 5 %10.4g) sets the format of the Nth value printed. If the format for a specific value has been set, it will take precedent over the *int* or *float* setting.

The *window* option sets the number of previous thermodynamic screen outputs over which thermo\_style custom ave quantities are averaged when printed.

**Restrictions:** none

**Related commands:**

thermo, thermo\_style, temperature

**Default:**

The option defaults are temp = default, lost = error, norm = yes for unit style of *lj*, norm = no for unit style of *real* and *metal*, flush = no, window = 10. The defaults for the line and format options depend on the thermo style. For styles "one", "granular", and "custom" the line and format defaults are "one", "%8d", and "%12.8g".



For style "multi", the line and format defaults are "multi", "%8d", and "%14.4f".

## thermo\_style command

### Syntax:

thermo\_style style args

- style = *one* or *multi* or *granular* or *custom*
- args = list of arguments for a particular style

```
one args = none
multi args = none
granular args = none
custom args = list of attributes
    possible attributes = step, atoms, cpu, temp, press, pe, ke, eng,
                        evdwl, ecoul, epair, ebond, eangle, edihed, eimp, emol, elong,
                        vol, lx, ly, lz, pxx, pyy, pzz, pxy, pxz, pyz
                        gke, grot, tave, pave, eave, peave, t_ID
    step = timestep
    atoms = # of atoms
    cpu = elapsed CPU time
    temp = temperature
    press = pressure
    pe = total potential energy
    ke = kinetic energy
    eng = total energy (pe + ke)
    evdwl = VanderWaal pairwise energy
    ecoul = Coulombic pairwise energy
    epair = pairwise (evdwl + ecoul)
    ebond = bond energy
    eangle = angle energy
    edihed = dihedral energy
    eimp = improper energy
    emol = molecular energy (ebond + eangle + edihed + eimp)
    elong = long-range kspace energy
    vol = volume
    lx,ly,lz = box lengths in x,y,z
    pxx,pyy,pzz,pxy,pxz,pyz = 6 components of pressure tensor
    gke = granular translational kinetic energy (without frozen atoms)
    grot = granular rotational kinetic energy (without frozen atoms)
    tave, pave, eave, peave = time-averaged temp, press, eng, pe
    t_ID = temperature as computed by temperature ID
```

### Examples:

```
thermo_style multi
thermo_style custom step temp pe eng press vol
thermo_style custom step temp t_left t_right eng
```

### Description:

Set the style in which thermodynamic data is printed to the screen and log file.

Style *one* prints a one–line summary of thermodynamic info that is the equivalent of "thermo\_style custom step temp epair emol eng press". The line contains only numeric values.

Style *multi* prints a multiple–line listing of thermodynamic info that is the equivalent of "thermo\_style custom eng ke temp pe ebond eangle edihed eimp evdwl ecoul elong press". The listing contains numeric values and a string ID for each quantity.

Style *granular* is used with atom\_style granular and prints a one–line numeric summary that is the equivalent of "thermo\_style custom step atoms gke grot".

Style *custom* is the most general setting and allows you to specify which of the quantities listed above you want printed on each thermodynamic timestep.

Also, all styles except *custom* have *vol* added to their list of outputs as a final printed quantity when the simulation box volume changes during the simulation.

All thermodynamic quantities which require a temperature *temp*, *press*, *ke*, *eng*, *tave*, *eave*, use the temperature with ID = *default* that is defined by LAMMPS (see the temperature command) that performs an average over all atoms. This can be changed via the thermo\_modify command. The exception is the *t\_ID* quantity which directly specifies which temperature to compute and print out.

The time–averaged quantities *tave*, *pave*, *eave*, *peave* are averaged over the last N thermodynamic outputs to the screen (not the last N timesteps), where N is the value set by the *window* option of the thermo\_modify command (N = 10 by default).

The *t\_ID* quantity allows for user–defined temperatures to be printed with thermodynamic output. For example, if either of the commands

```
temperature mine all region sphere
fix mine all temp/rescale 100 1.0 1.0 0.1 1.0 region sphere
```

were used to compute or thermostat the temperature of atoms inside a spherical geometric region, then the keyword *t\_mine* will print that temperature as part of thermodynamic output.

Some fixes also generate quantities that can be appended to these lists each time thermodynamic info prints out, if enabled by the fix\_modify command. See individual fix commands for more details, e.g. the fix nvt and fix npt commands.

Options invoked by the thermo\_modify command can be used to set the one– or multi–line format of the print–out, the normalization of energy quantities (total or per–atom), and the numeric precision of each printed value.

### Restrictions:

Atom style granular cannot compute the usual temperature and pressure settings because it stores atom masses differently. The gke and grot settings should be used instead (or use thermo style granular).

This command must come after the simulation box is defined by a read\_data, read\_restart, or create\_box command.

### Related commands:

thermo\_style command

[thermo](#), [thermo\\_modify](#), [fix\\_modify](#), [temperature](#)

**Default:**

`thermo_style one`

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## timestep command

**Syntax:**

`timestep dt`

- `dt` = timestep size (time units)

**Examples:**

```
timestep 2.0
timestep 0.003
```

**Description:**

Set the timestep size for subsequent molecular dynamics simulations. See the [units](#) command for a discussion of time units. Note that using the `units` command also sets the timestep to its default value in the chosen units.

When the run style is *respa*, `dt` is the timestep for the outer loop (largest) timestep.

**Restrictions:** none

**Related commands:**

[run](#), [run\\_style](#) *respa*, [units](#)

**Default:**

```
timestep = 0.005 tau for units = lj
timestep = 1.0 fmsec for units = real
timestep = 0.001 psec for units = metal
```

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## undump command

**Syntax:**

`undump dump-ID`

- `dump-ID` = ID of previously defined dump

**Examples:**

timestep command

```
undump mine
undump 2
```

**Description:**

Turn off a previously defined dump so that it is no longer active. This closes the file associated with the dump.

**Restrictions:** none

**Related commands:**

[dump](#)

**Default:** none

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## unfix command

**Syntax:**

```
unfix fix-ID
```

- fix-ID = ID of a previously defined fix

**Examples:**

```
unfix 2
unfix lower-boundary
```

**Description:**

Turn off a fix that was previously defined with a [fix](#) command.

**Restrictions:** none

**Related commands:**

[fix](#)

**Default:** none

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## units command

**Syntax:**

```
units style
```

- style = *lj* or *real* or *metal*

### Examples:

```
units metal
units lj
```

### Description:

This command sets the style of units used for a simulation. It determines the units of all quantities specified in the input script and data file, as well as quantities output to the screen, log file, and dump files. Typically, this command is used at the very beginning of an input script.

For style *lj*, all quantities are unitless:

- distance = sigma
- time = tau
- mass = one
- energy = epsilon
- velocity = sigma/tau
- force = epsilon/sigma
- temperature = reduced LJ temperature
- pressure = reduced LJ pressure
- charge = reduced LJ charge
- electric field = force/charge

For style *real*, these are the units:

- distance = Angstroms
- time = femtoseconds
- mass = grams/mole
- energy = Kcal/mole
- velocity = Angstroms/femtosecond
- force = Kcal/mole–Angstrom
- temperature = degrees K
- pressure = atmospheres
- charge = multiple of electron charge (+1.0 is a proton)
- electric field = volts/Angstrom

For style *metal*, these are the units:

- distance = Angstroms
- time = picoseconds
- mass = grams/mole
- energy = eV
- velocity = Angstroms/picosecond
- force = eV/Angstrom
- temperature = degrees K
- pressure = bars
- charge = multiple of electron charge (+1.0 is a proton)
- electric field = volts/Angstrom

This command also sets the timestep size and neighbor skin distance to default values for each style. For style *lj* these are  $dt = 0.005 \tau$  and  $skin = 0.3 \sigma$ . For style *real* these are  $dt = 1.0 \text{ fmsec}$  and  $skin = 2.0 \text{ Angstroms}$ . For style *metal* these are  $dt = 0.001 \text{ psec}$  and  $skin = 2.0 \text{ Angstroms}$ .

### Restrictions:

This command cannot be used after the simulation box is defined by a [read\\_data](#) or [create\\_box](#) command.

**Related commands:** none

### Default:

units lj

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## variable command

### Syntax:

variable name style args ...

- name = single lower-case character, 'a' thru 'z'
- style = *index* or *loop* or *equal* or *world* or *universe*

*index* args = one or more strings  
*loop* args = N = integer size of loop  
*equal* args = one string containing functions, vectors, keywords, numbers  
    functions = add(x,y), sub(x,y), mult(x,y), div(x,y), neg(x), pow(x,y), exp(x), ln(x)  
    vectors = x[5], y[12], z[17], vx[88], vy[19], vz[2], fx[1], fy[2005], fz[1]  
    keywords = same keywords (mostly) as in [thermo style custom](#) command  
*world* args = one string for each partition of processors  
*universe* args = one or more strings

### Examples:

```
variable x index run1 run2 run3 run4 run5 run6 run7 run8
variable a loop 20
variable b equal div(temp,3.0)
variable b equal add(x[234],mult(0.5,lx))
variable t world 300.0 310.0 320.0 330.0
variable x universe 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
```

### Description:

This command assigns one or more values to a variable name so that the variable can be used in subsequent input script commands. In this context a "value" is a string which could be text or numbers, as in the examples above. As explained in [this section](#), occurrences of \$X in an input script line are replaced by the variable's value, where X is a single lower-case character from "a" to "z".

As described below, for variable styles *index*, *loop*, and *universe*, the value assigned to a variable can be incremented via the [next](#) command. When there are no more values to assign, the variable is "exhausted" and a flag is set that causes the next [jump](#) command encountered in the input script to be skipped. This enables the

construction of simple loops in the input script that are iterated over and exited from.

When a variable command is encountered for a variable that has already been specified, the command is skipped. This is the case for all variable styles except *equal*, so that *equal*-style variable names can be re-used and re-defined anytime. Skipping allows you to loop over the same input script many times without re-defining your variables. When a variable is exhausted via the next command, it is then available to be re-defined in a subsequent variable command.

For the *index* style, one or more strings are specified. Initially, the 1st string is assigned to the variable. Each time a next command is used with the variable name, the next string is assigned. All processors assign the same string to the variable. *Index*-style variables can also be set (with a single value) by using the command-line switch `-var`; see this section for details.

The *loop* style is identical to the *index* style except that the strings are the integers from 1 to N. Initially, the string "1" is assigned to the variable. Each time a next command is used with the variable name, the next string ("2", "3", etc) is assigned. All processors assign the same string to the variable.

For the *equal* style, a single string is specified which represents an equation that will be evaluated afresh each time the variable is used. Thus the variable can take on different values at different stages of the input script. For example, if the variable is used in a fix print command, it could print different values each timestep it was invoked. The next command cannot be used with *equal*-style variables, since there is only one value. Note that, as with any other input script command, it is feasible to use another variable in the *equal* variable's string, e.g. variable `y` equal `mult($x,2)`. However, `$x` will be replaced immediately by it's current value when the command is first parsed, not each time that `$y` is substituted for.

The syntax of the equation assigned to *equal* variables is simple. It can contain "functions", "vectors", "keywords", or "numbers" in any combination.

- Function = a keyword followed by parenthesis with one or two arguments
- Supported functions = `add(x,y)`, `sub(x,y)`, `mult(x,y)`, `div(x,y)`, `neg(x)`, `pow(x,y)`, `exp(x)`, `ln(x)`
- Example function usage = `div(1.0e20,3.0)`, `neg(x[34])`, `pow(lx,3.0)`
- Vector = a keyword followed by square brackets containing an atom ID
- Supported vectors = `x`, `y`, `z`, `vx`, `vy`, `vz`, `fx`, `fy`, `fz`
- Example vector usage = `x[123]`, `fz[1000]`
- Keyword = keywords supported by the thermo style custom command except `cpu` and pressure tensor components (`pxx`, `pyy`, etc)
- Supported keywords = `step`, `atoms`, `temp`, `press`, `pe`, `ke`, `eng`, `evdwl`, `ecoul`, `epair`, `ebond`, `eangle`, `edihed`, `eimp`, `emol`, `elong`, `vol`, `lx`, `ly`, `lz`, `gke`, `grot`, `t_ID`
- Example keyword usage = `atoms`, `pow(vol,0.333)`, `mult(elong,0.5)`
- Number = `0.2`, `1.0e20`, `-15.4`, etc

Keywords have restrictions on when they can be assigned to variables. For example, keywords that compute thermodynamic quantities can only be invoked after the first simulation has begun. A warning is issued if thermodynamic keywords are invoked on timesteps when thermodynamic information is not being printed to the screen, since the values assigned to the variable may be out-of-date.

The variable *equal* equation can also be nested in that function arguments can be functions, vectors, keywords, or numbers. For example, this is a valid equation:

```
variable x equal div(add(pe,ke),pow(vol,div(1,3)))
```

For the *world* style, one or more strings are specified. There must be one string for each processor partition or "world". See [this section](#) of the manual for information on running LAMMPS with multiple partitions via the "-partition" command-line switch. This variable command assigns one string to each world. All processors in the world are assigned the same string. The next command cannot be used with *equal*-style variables, since there is only one value per world. This style of variable is useful when you wish to run different simulations on different partitions, or when performing a parallel tempering simulation (see the [temper](#) command), to assign different temperatures to different partitions.

For the *universe* style, one or more strings are specified. There must be at least as many strings as there are processor partitions or "worlds". See [this page](#) for information on running LAMMPS with multiple partitions via the "-partition" command-line switch. This variable command initially assigns one string to each world. When a [next](#) command is encountered using this variable, the first processor partition to encounter it, is assigned the next available value. This continues until all the variable values are consumed. Thus, this command can be used to run 50 simulations on 8 processor partitions. The simulations will be run one after the other on whatever partition becomes available, until they are all finished. *Universe*-style variables are incremented using the files "tmp.lammps.variable" and "tmp.lammps.variable.lock" which you will see in your directory during such a LAMMPS run.

If a variable command is encountered when the variable has already been defined, the command is ignored. This allows an input script with a variable command to be processed multiple times; see the [jump](#) or [include](#) commands. It also means that the use of the command-line switch -var will override a corresponding variable setting in the input script.

#### Restrictions:

The use of atom vectors in *equal* style variables requires the atom style to use a global mapping in order to look up the vector indices. Only atom styles with molecular information create global maps.

#### Related commands:

[next](#), [jump](#), [include](#), [temper](#), [fix print](#), [print](#)

**Default:** none

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## velocity command

### Syntax:

```
velocity group-ID style args keyword value ...
```

- group-ID = ID of group of atoms whose velocity will be changed
- style = *create* or *set* or *scale* or *ramp* or *zero*

```
create args = temp seed
    temp = temperature value (temperature units)
    seed = random # seed (8 digits or less)
set args = vx vy vz
    vx,vy,vz = velocity value or NULL (velocity units)
scale args = temp
    temp = temperature value (temperature units)
```



```

ramp args = vdim vlo vhi dim clo chi
vdim = vx or vy or vz
vlo,vhi = lower and upper velocity value (velocity units)
dim = x or y or z
clo,chi = lower and upper coordinate bound (distance units)
zero args = linear or angular
linear = zero the linear momentum
angular = zero the angular momentum

```

- zero or more keyword/value pairs may be appended to the args
- keyword = *dist* or *sum* or *mom* or *rot* or *temp* or *loop* or *units*

```

dist value = uniform or gaussian
sum value = no or yes
mom value = no or yes
rot value = no or yes
temp value = temperature ID
loop value = all or local or geom
units value = box or lattice

```

### Examples:

```

velocity all create 300.0 4928459 rot yes dist gaussian
velocity border set NULL 4.0 3.0 sum yes units box
velocity flow scale 300.0
velocity flow ramp lattice vx 0.0 5.0 y 5 20 temp mytemp
velocity all zero linear

```

### Description:

Set or change the velocities of a group of atoms in one of several styles. For each style, there are required arguments and optional keyword/value parameters. Not all options are used by each style. Each option has a default as listed below.

The *create* style generates an ensemble of velocities using a random number generator with the specified seed as the specified temperature.

The *set* style sets the velocities of all atoms in the group to the specified values. If any component is specified as NULL, then it is not set.

The *scale* style computes the current temperature of the group of atoms and then rescales the velocities to the specified temperature.

The *ramp* style is similar to that used by the temperature ramp command. Velocities ramped uniformly from vlo to vhi are applied to dimension vx, or vy, or vz. The value assigned to a particular atom depends on its relative coordinate value (in dim) from clo to chi. For the example above, an atom with y-coordinate of 10 (1/4 of the way from 5 to 20), would be assigned a x-velocity of 1.25 (1/4 of the way from 0.0 to 5.0). Atoms outside the coordinate bounds (less than 5 or greater than 20 in this case), are assigned velocities equal to vlo or vhi (0.0 or 5.0 in this case).

The *zero* style adjusts the velocities of the group of atoms so that the aggregate linear or angular momentum is zero. No other changes are made to the velocities of the atoms.

All temperatures specified in the velocity command are in temperature units; see the units command. The units of velocities and coordinates depend on whether the *units* keyword is set to *box* or *lattice*, as discussed

below.

The keyword/value option pairs are used in the following ways by the various styles.

The *dist* option is used by *create*. The ensemble of generated velocities can be a *uniform* distribution from some minimum to maximum value, scaled to produce the requested temperature. Or it can be a *gaussian* distribution with a mean of 0.0 and a sigma scaled to produce the requested temperature.

The *sum* option is used by all styles, except *zero*. The new velocities will be added to the existing ones if sum = yes, or will replace them if sum = no.

The *mom* and *rot* options are used by *create*. If mom = yes, the linear momentum of the newly created ensemble of velocities is zeroed; if rot = yes, the angular momentum is zeroed.

The *temp* option is used by *create* and *scale* to specify a user-defined way of computing temperature. If this option is not used, *create* and *scale* compute temperature with the style "full" for the group of atoms whose velocity is being altered. See the [temperature](#) command for details. If the computed temperature should have degrees-of-freedom removed due to fix constraints (e.g. SHAKE or rigid-body constraints), then the appropriate fix command must be specified before the velocity command is issued.

The *loop* option is used by *create*. If loop = all, then each processor loops over all atoms in the simulation to create velocities, but only stores velocities for atoms it owns. This can be a slow loop for a large simulation. It will produce the same set of velocities, independent of the number of processors, if atoms were read from a data file. It will not produce such independent velocities if atoms were created using the [create\\_atoms](#) command. If loop = local, then each processor loops over only its atoms to produce velocities. The random number seed is adjusted to give a different set of velocities on each processor. This is a fast loop, but will always produce different sets of velocities when a simulation is run on a different number of processors. If loop = geom, then each processor loops over only its atoms. For each atom a unique random number seed is created, based on the atom's xyz coordinates. A velocity is generated using that seed. This is a fast loop and will always give the same set of velocities, independent of how many processors are used. However, the generated velocities may be more correlated than if the *all* or *local* options are used. Note that the *loop geom* option will not necessarily assign identical velocities for two simulations run on different machines. This is because the computations based on xyz coordinates are sensitive to tiny differences in the double-precision value for a coordinate as stored on a particular machine.

The *units* option is used by *set* and *ramp*. If units = box, the velocities and coordinates specified in the velocity command are in the standard units described by the [units](#) command (e.g. Angstroms/fmsec for real units). If units = lattice, velocities are in units of lattice spacings per time (e.g. spacings/fmsec) and coordinates are in lattice spacings. The [lattice](#) command must have been previously used to define the lattice spacing.

For all styles, no atoms are assigned z-component velocities if the simulation is 2d; see the [dimension](#) command.

**Restrictions:** none

**Related commands:**

[fix shake](#), [lattice](#)

**Default:**

velocity command

The option defaults are dist = uniform, sum = no, mom = yes, rot = no, temp = full style on group-ID, loop = all, and units = lattice.

## write\_restart command

### Syntax:

```
write_restart file
```

- file = name of file to write restart information to

### Examples:

```
write_restart restart.equil
```

### Description:

Write a binary restart file of the current state of the simulation. See the [read\\_restart](#) command for information about what is stored in a restart file.

During a long simulation, the [restart](#) command is typically used to dump restart files periodically. The write\_restart command is useful after a minimization or whenever you wish to write out a single current restart file.

Restart files can be read by a [read\\_restart](#) command to restart a simulation from a particular state. Because the file is binary (to enable exact restarts), it may not be readable on another machine. In this case, the restart2data program in the tools directory can be used to convert a restart file to an ASCII data file.

### Restrictions:

This command requires inter-processor communication to migrate atoms before the restart file is written. This means that your system must be ready to perform a simulation before using this command (force fields setup, atom masses set, etc).

### Related commands:

[restart](#), [read\\_restart](#)

**Default:** none